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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:21:13 ; Search time 214.344 Seconds
(without alignments)
684.218 Million cell updates/sec

Title: US-10-517-956-1

Perfect score: 1817
Sequence: 1 METNFTPLNXYEVEYSESA.....TMDTANASAPPAETELQAM 351

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
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5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1817	100.0	351	3 US-09-944-807-2	Sequence 2, Appl1
2	1817	100.0	351	4 US-10-225-567A-120	Sequence 120, App
3	1817	100.0	351	5 US-10-874-015-2	Sequence 2, Appl1
4	1817	100.0	351	5 US-10-482-029-263	Sequence 263, App
5	1817	100.0	351	5 US-10-509-715-2	Sequence 2, Appl1
6	1817	100.0	351	5 US-10-517-956-1	Sequence 1, Appl1
7	1811	99.7	351	3 US-09-826-509-501	Sequence 501, App
8	1811	99.7	351	3 US-10-925-095-501	Sequence 501, App
9	1420	78.2	351	5 US-10-517-956-12	Sequence 12, Appl
10	1419	78.2	351	5 US-10-517-956-10	Sequence 10, Appl
11	1327	73.0	581	5 US-10-505-486-118	Sequence 118, App
12	1318	72.5	353	4 US-10-225-567A-633	Sequence 633, App
13	1318	72.5	353	4 US-10-116-875-218	Sequence 218, App
14	1318	72.5	353	4 US-10-789-241-12	Sequence 12, Appl
15	1318	72.5	353	4 US-10-517-956-14	Sequence 14, Appl
16	1304	71.8	349	4 US-10-305-555-8	Sequence 8, Appl1
17	1250.5	68.8	350	4 US-10-325-567A-631	Sequence 631, App
18	1250.5	68.8	350	4 US-10-354-358-2	Sequence 2, Appl1
19	1244.5	68.5	350	3 US-09-826-509-499	Sequence 499, App
20	1244.5	68.5	350	3 US-10-925-095-499	Sequence 499, App
21	1243.5	68.4	351	5 US-09-893-512-16	Sequence 16, Appl
22	1243.5	68.4	351	5 US-10-799-736-16	Sequence 16, Appl
23	1174.5	64.6	354	3 US-09-867-669-11	Sequence 11, Appl
24	1174.5	64.6	354	3 US-10-218-574-11	Sequence 11, Appl
25	1174.5	64.6	354	5 US-10-984-898-11	Sequence 11, Appl
26	1157.5	63.7	343	3 US-09-879-017-2	Sequence 2, Appl1
27	1107.5	61.0	323	4 US-10-005-196-2	Sequence 2, Appl1

28	1107.5	61.0	323	4 US-10-026-937-2	Sequence 2, Appl1
29	554.5	30.5	356	4 US-10-251-385-246	Sequence 246, App
30	554	30.5	594	5 US-10-505-486-119	Sequence 119, App
31	553.5	30.5	342	4 US-10-226-102-4	Sequence 4, Appl1
32	553.5	30.5	342	4 US-10-407-079-4	Sequence 4, Appl1
33	553.5	30.5	356	4 US-10-226-102-2	Sequence 2, Appl1
34	553.5	30.5	356	4 US-10-226-102-17	Sequence 17, App
35	553.5	30.5	356	4 US-10-251-385-270	Sequence 270, App
36	553.5	30.5	356	4 US-10-225-567A-484	Sequence 484, App
37	553.5	30.5	356	4 US-10-407-079-2	Sequence 2, Appl1
38	553.5	30.5	356	4 US-10-407-079-17	Sequence 17, Appl
39	553.5	30.5	356	5 US-10-684-206-4	Sequence 4, Appl1
40	553.5	30.5	390	4 US-10-017-161-760	Sequence 760, App
41	542.5	29.9	477	3 US-09-892-206-2	Sequence 2, Appl1
42	542.5	29.9	477	4 US-10-764-649-10	Sequence 10, Appl
43	542.5	29.9	477	6 US-11-046-857-4	Sequence 4, Appl1
44	538.5	29.6	371	3 US-09-905-253A-4	Sequence 4, Appl1
45	538.5	29.6	371	4 US-10-201-187-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-944-807-2
Sequence 2, Application US/09944807
Patent No. US20020119494A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim Pharma KG
TITLE OF INVENTION: Method for identifying substances which positively
TITLE OF INVENTION: Influence inflammatory conditions of chronic
FILE REFERENCE: 082 00n
CURRENT APPLICATION NUMBER: US/09/944, 807
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: UK 0021484.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 351
TYPE: PRT
ORGANISM: Homo sapiens
US-09-944-807-2

Query Match 100.0%; Score 1817; DB 3; Length 351;
Best Local Similarity 100.0%; Pred. No. 2.9e-148; Indels 0; Gaps 0;
Matches 351; Conservative 0; Mismatches 0;

Qy	1	METNFTPLNXYEVEYSAGYTVLRILPLVVLGVTVLGVGLNGGLVWVAGFRMTRTVT	60
Db	1	METNFTPLNXYEVEYSAGYTVLRILPLVVLGVTVLGVGLNGGLVWVAGFRMTRTVT	60
Qy	61	TTCTYMLALADSFSTATLPLILVSNMAGKWPGLCKLIHIVDINLFGSVFLIGFLA	120
Db	61	TTCTYMLALADSFSTATLPLILVSNMAGKWPGLCKLIHIVDINLFGSVFLIGFLA	120
Qy	121	LDRCTVLAHPWAQNRRTYSLMKYIVGPMIALVTLFVPLFELTVTIPNGDTYCTFNP	180
Db	121	LDRCTVLAHPWAQNRRTYSLMKYIVGPMIALVTLFVPLFELTVTIPNGDTYCTFNP	180
Qy	181	ASWGTPERLKVATLMTARGLIRFVIGFSLPMSIVAICYGLIAKIKKGMKISRP	240
Db	181	ASWGTPERLKVATLMTARGLIRFVIGFSLPMSIVAICYGLIAKIKKGMKISRP	240
Qy	241	RVLTAVVASFFTCWPFQVALIGTVMLKEMLPYGRYKIIDILVNFTSSLAFNSCLNPM	300
Db	241	RVLTAVVASFFTCWPFQVALIGTVMLKEMLPYGRYKIIDILVNFTSSLAFNSCLNPM	300
Qy	301	LVYFVQDPRRLHSLPTSLRALSDESAPTNDTANASAPPAETELQAM 351	
Db	301	LVYFVQDPRRLHSLPTSLRALSDESAPTNDTANASAPPAETELQAM 351	

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RESULT 2
US-10-225-567A-120
/ Sequence 120, Application US/10225567A
/ Publication No. US20030113798A1
/ GENERAL INFORMATION:
/ APPLICANT: Lifespan Biociences
/ APPLICANT: Brown, Joseph P.
/ APPLICANT: Burner, Glenn C.
/ APPLICANT: Roush, Christine L.
/ TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
/ FILE REFERENCE: 1920-4-4
/ CURRENT APPLICATION NUMBER: US/10/225,567A
/ CURRENT FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 60/257,144
/ PRIOR FILING DATE: 2000-12-19
/ NUMBER OF SEQ ID NOS: 2292
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 120
/ LENGTH: 351
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-10-225-567A-120

Query Match      100.0%; Score 1817; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 2.9e-148;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEXEYEVESAGYTVLRILPLVVGTVFVLGNGLVIVWAGFRMTRTYT 60
DB 1 METNFTPLNEXEYEVESAGYTVLRILPLVVGTVFVLGNGLVIVWAGFRMTRTYT 60
QY 61 TICYNLALADSFATLPFLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVFLIGFLA 120
DB 61 TICYNLALADSFATLPFLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVFLIGFLA 120
QY 121 LDRICVLAHPVWAQNHRVSLAMKVI VGPWIALVLTLPVFLFTVTIIPNGDTYCTENF 180
DB 121 LDRICVLAHPVWAQNHRVSLAMKVI VGPWIALVLTLPVFLFTVTIIPNGDTYCTENF 180
QY 181 ASWGCTPEERLKVAITMTLARGIIRFVIGFSLPMSIVACYGLIAKIHKKGMIKSSRPL 240
DB 181 ASWGCTPEERLKVAITMTLARGIIRFVIGFSLPMSIVACYGLIAKIHKKGMIKSSRPL 240
QY 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYKRYKIIDLIVNPTSSIAFPNSCLNPM 300
DB 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYKRYKIIDLIVNPTSSIAFPNSCLNPM 300
QY 301 LVFVGGDFRERLIHSLPTSLERALSDESAPTNDTAANSASPAETELQAM 351
DB 301 LVFVGGDFRERLIHSLPTSLERALSDESAPTNDTAANSASPAETELQAM 351

RESULT 3
US-10-874-015-2
/ Sequence 2, Application US/10874015
/ Publication No. US2004023630A1
/ GENERAL INFORMATION:
/ APPLICANT: Jung, Birgit
/ APPLICANT: Kraut, Norbert
/ APPLICANT: Mueller, Stefan
/ APPLICANT: Kistler, Barbara
/ APPLICANT: Seicher, Peter
/ APPLICANT: Quast, Karen
/ APPLICANT: Welch, Andreas
/ TITLE OF INVENTION: Method for identifying substances which positively
/ TITLE OF INVENTION: influence inflammatory conditions of chronic
/ TITLE OF INVENTION: inflammatory airway diseases
/ FILE REFERENCE: 1/1144-1-D1
/ CURRENT APPLICATION NUMBER: US/10/874,015
/ CURRENT FILING DATE: 2004-06-22
/ PRIOR APPLICATION NUMBER: UK 0021484.1
/ PRIOR FILING DATE: 2000-09-01
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NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 351
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-10-874-015-2

Query Match      100.0%; Score 1817; DB 5; Length 351;
Best Local Similarity 100.0%; Pred. No. 2.9e-148;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEXEYEVESAGYTVLRILPLVVGTVFVLGNGLVIVWAGFRMTRTYT 60
DB 1 METNFTPLNEXEYEVESAGYTVLRILPLVVGTVFVLGNGLVIVWAGFRMTRTYT 60
QY 61 TICYNLALADSFATLPFLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVFLIGFLA 120
DB 61 TICYNLALADSFATLPFLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVFLIGFLA 120
QY 121 LDRICVLAHPVWAQNHRVSLAMKVI VGPWIALVLTLPVFLFTVTIIPNGDTYCTENF 180
DB 121 LDRICVLAHPVWAQNHRVSLAMKVI VGPWIALVLTLPVFLFTVTIIPNGDTYCTENF 180
QY 181 ASWGCTPEERLKVAITMTLARGIIRFVIGFSLPMSIVACYGLIAKIHKKGMIKSSRPL 240
DB 181 ASWGCTPEERLKVAITMTLARGIIRFVIGFSLPMSIVACYGLIAKIHKKGMIKSSRPL 240
QY 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYKRYKIIDLIVNPTSSIAFPNSCLNPM 300
DB 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYKRYKIIDLIVNPTSSIAFPNSCLNPM 300
QY 301 LVFVGGDFRERLIHSLPTSLERALSDESAPTNDTAANSASPAETELQAM 351
DB 301 LVFVGGDFRERLIHSLPTSLERALSDESAPTNDTAANSASPAETELQAM 351

RESULT 4
US-10-482-029-263
/ Sequence 263, Application US/10482029
/ Publication No. US20050037445A1
/ GENERAL INFORMATION:
/ APPLICANT: ODIN medical A/S
/ TITLE OF INVENTION: Oncology drug innovation
/ FILE REFERENCE: P 573 PC00
/ CURRENT APPLICATION NUMBER: US/10/482,029
/ CURRENT FILING DATE: 2003-12-29
/ NUMBER OF SEQ ID NOS: 437
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 263
/ LENGTH: 351
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-10-482-029-263

Query Match      100.0%; Score 1817; DB 5; Length 351;
Best Local Similarity 100.0%; Pred. No. 2.9e-148;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEXEYEVESAGYTVLRILPLVVGTVFVLGNGLVIVWAGFRMTRTYT 60
DB 1 METNFTPLNEXEYEVESAGYTVLRILPLVVGTVFVLGNGLVIVWAGFRMTRTYT 60
QY 61 TICYNLALADSFATLPFLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVFLIGFLA 120
DB 61 TICYNLALADSFATLPFLIVSMAMGKMPFGMFLCKLHIIVDINLFGSVFLIGFLA 120
QY 121 LDRICVLAHPVWAQNHRVSLAMKVI VGPWIALVLTLPVFLFTVTIIPNGDTYCTENF 180
DB 121 LDRICVLAHPVWAQNHRVSLAMKVI VGPWIALVLTLPVFLFTVTIIPNGDTYCTENF 180
QY 181 ASWGCTPEERLKVAITMTLARGIIRFVIGFSLPMSIVACYGLIAKIHKKGMIKSSRPL 240
DB 181 ASWGCTPEERLKVAITMTLARGIIRFVIGFSLPMSIVACYGLIAKIHKKGMIKSSRPL 240
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Db 181 ASWGTPBERLKAITMLTARGIIRFYIGSLPMSIYALCYGLIAAKIHKKMKISRL 240
 QY 241 RVLTAIVASFFICMPFPQVALLGTWMLKEMLFYGYKXIIDIIVNPTSSIAFPNSCLNPM 300
 Db 241 RVLTAIVASFFICMPFPQVALLGTWMLKEMLFYGYKXIIDIIVNPTSSIAFPNSCLNPM 300
 QY 301 LYYFVGDFRERLIHSLPTSLERALSDESAPTNDTANASPPAETELQAM 351
 Db 301 LYYFVGDFRERLIHSLPTSLERALSDESAPTNDTANASPPAETELQAM 351

RESULT 5

US-10-509-715-2
 ; Sequence 2, Application US/10509715
 ; Publication No. US20050164305A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goiz, Stefan
 ; APPLICANT: Brugemeier, Ulf
 ; APPLICANT: Geerts, Andreas
 ; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
 ; TITLE OF INVENTION: N-Formyl Peptide Receptor Like 1 (FPR1)
 ; FILE REFERENCE: Le A 35 949
 ; CURRENT APPLICATION NUMBER: US/10/509, 715
 ; CURRENT FILING DATE: 2004-10-01
 ; PRIOR APPLICATION NUMBER: PCT/EP03/02959
 ; PRIOR FILING DATE: 2003-03-21
 ; PRIOR APPLICATION NUMBER: EP 02007291.4
 ; PRIOR FILING DATE: 2002-04-03
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Patent version 3.3
 ; SEQ ID NO 2
 ; LENGTH: 351
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-509-715-2

Query Match 100.0%; Score 1817; DB 5; Length 351;
 Best Local Similarity 100.0%; Pred. No. 2.9e-148;
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEXEVSYESAGYTVLRILPLVVLGTVFVLGVLNGVIVWAGFRMTRTYT 60
 Db 1 METNFTPLNEXEVSYESAGYTVLRILPLVVLGTVFVLGVLNGVIVWAGFRMTRTYT 60
 QY 61 TICVLMALADFSFTATLPLIVSMAMGKMPGKFLCKLIHVVDINLFGSVFLIGFIA 120
 Db 61 TICVLMALADFSFTATLPLIVSMAMGKMPGKFLCKLIHVVDINLFGSVFLIGFIA 120
 QY 121 LDRICVLAHPVMAQNHRVTSIAKVIIVGPWIALVTLVPVFLPTVTIPNGDYCTFNF 180
 Db 121 LDRICVLAHPVMAQNHRVTSIAKVIIVGPWIALVTLVPVFLPTVTIPNGDYCTFNF 180
 QY 181 ASWGTPBERLKAITMLTARGIIRFYIGSLPMSIYALCYGLIAAKIHKKMKISRL 240
 Db 181 ASWGTPBERLKAITMLTARGIIRFYIGSLPMSIYALCYGLIAAKIHKKMKISRL 240
 QY 241 RVLTAIVASFFICMPFPQVALLGTWMLKEMLFYGYKXIIDIIVNPTSSIAFPNSCLNPM 300
 Db 241 RVLTAIVASFFICMPFPQVALLGTWMLKEMLFYGYKXIIDIIVNPTSSIAFPNSCLNPM 300
 QY 301 LYYFVGDFRERLIHSLPTSLERALSDESAPTNDTANASPPAETELQAM 351
 Db 301 LYYFVGDFRERLIHSLPTSLERALSDESAPTNDTANASPPAETELQAM 351

RESULT 6

US-10-517-956-1
 ; Sequence 1, Application US/10517956
 ; Publication No. US2005023326A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Takeda Chemical Industries, Ltd.
 ; TITLE OF INVENTION: Novel Screening Method
 ; FILE REFERENCE: 3067WOOP

; CURRENT APPLICATION NUMBER: US/10/517, 956
 ; CURRENT FILING DATE: 2004-12-13
 ; PRIOR APPLICATION NUMBER: JP 2002-173798
 ; PRIOR FILING DATE: 2002-06-14
 ; PRIOR APPLICATION NUMBER: JP 2002-205470
 ; PRIOR FILING DATE: 2002-07-15
 ; NUMBER OF SEQ ID NOS: 24
 ; SEQ ID NO 1
 ; LENGTH: 351
 ; TYPE: PRT
 ; ORGANISM: Human
 US-10-517-956-1

Query Match 100.0%; Score 1817; DB 5; Length 351;
 Best Local Similarity 100.0%; Pred. No. 2.9e-148;
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEXEVSYESAGYTVLRILPLVVLGTVFVLGVLNGVIVWAGFRMTRTYT 60
 Db 1 METNFTPLNEXEVSYESAGYTVLRILPLVVLGTVFVLGVLNGVIVWAGFRMTRTYT 60
 QY 61 TICVLMALADFSFTATLPLIVSMAMGKMPGKFLCKLIHVVDINLFGSVFLIGFIA 120
 Db 61 TICVLMALADFSFTATLPLIVSMAMGKMPGKFLCKLIHVVDINLFGSVFLIGFIA 120
 QY 121 LDRICVLAHPVMAQNHRVTSIAKVIIVGPWIALVTLVPVFLPTVTIPNGDYCTFNF 180
 Db 121 LDRICVLAHPVMAQNHRVTSIAKVIIVGPWIALVTLVPVFLPTVTIPNGDYCTFNF 180
 QY 181 ASWGTPBERLKAITMLTARGIIRFYIGSLPMSIYALCYGLIAAKIHKKMKISRL 240
 Db 181 ASWGTPBERLKAITMLTARGIIRFYIGSLPMSIYALCYGLIAAKIHKKMKISRL 240
 QY 241 RVLTAIVASFFICMPFPQVALLGTWMLKEMLFYGYKXIIDIIVNPTSSIAFPNSCLNPM 300
 Db 241 RVLTAIVASFFICMPFPQVALLGTWMLKEMLFYGYKXIIDIIVNPTSSIAFPNSCLNPM 300
 QY 301 LYYFVGDFRERLIHSLPTSLERALSDESAPTNDTANASPPAETELQAM 351
 Db 301 LYYFVGDFRERLIHSLPTSLERALSDESAPTNDTANASPPAETELQAM 351

RESULT 7

US-09-826-509-501
 ; Sequence 501, Application US/09826509
 ; Publication No. US20030204073A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lehmann-Bruhnsma, Karin
 ; APPLICANT: Liaw, Chen W.
 ; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
 ; TITLE OF INVENTION: Protein-coupled Receptors
 ; FILE REFERENCE: ALEN-207
 ; CURRENT APPLICATION NUMBER: US/09/826, 509
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/195, 747
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: 09/170, 496
 ; PRIOR FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 589
 ; SOFTWARE: Patent version 2.1
 ; SEQ ID NO 501
 ; LENGTH: 351
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-826-509-501

Query Match 99.7%; Score 1811; DB 3; Length 351;
 Best Local Similarity 99.7%; Pred. No. 9.6e-148;
 Matches 350; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 METNFTPLNEXEVSYESAGYTVLRILPLVVLGTVFVLGVLNGVIVWAGFRMTRTYT 60

Db 1 METNFTPLMBEVSYESAGYTVLRILPLVLGVTFVLGVLGNGLVIVWAGFRMRTVT 60
Qy 61 TICYLNLALADFSFTATLPPLIVSMANGKMPGPFCKLHIYVDINLFGSVPLIGFIA 120
Db 61 TICYLNLALADFSFTATLPPLIVSMANGKMPGPFCKLHIYVDINLFGSVPLIGFIA 120
Qy 121 LDRICICVLHPVMAQNHRVTSIAKVIIVGPWILAVLTPVPLFTVTITPNGDYCTCFNF 180
Db 121 LDRICICVLHPVMAQNHRVTSIAKVIIVGPWILAVLTPVPLFTVTITPNGDYCTCFNF 180
Qy 181 ASWGTPEERBLKVAITMLTARGIIRFVIGFSLPMSIYACGLIAAKIHKKMKISSRPL 240
Db 181 ASWGTPEERBLKVAITMLTARGIIRFVIGFSLPMSIYACGLIAAKIHKKMKISSRPL 240
Qy 241 RVLTAVVASFFICWPFQVALLGTWVKEMLFYGYKKIIDILVNPTSSIAFNSCLNPM 300
Db 241 RVLTAVVASFFICWPFQVALLGTWVKEMLFYGYKKIIDILVNPTSSIAFNSCLNPM 300
Qy 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPAPTNDTAANSASPAETELQAM 351
Db 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPAPTNDTAANSASPAETELQAM 351

RESULT 8

US-10-925-095-501
; Sequence 501, Application US/10925095
; Publication No. US20050019840A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruhnsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/10/925, 095
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826, 509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195, 747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170, 496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 501
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-925-095-501

Query Match 99.7%; Score 1811; DB 5; Length 351;

Best Local Similarity 99.7%; Pred. No. 9.6e-148;

Matches 350; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 METNFTPLMBEVSYESAGYTVLRILPLVLGVTFVLGVLGNGLVIVWAGFRMRTVT 60
Db 1 METNFTPLMBEVSYESAGYTVLRILPLVLGVTFVLGVLGNGLVIVWAGFRMRTVT 60
Qy 61 TICYLNLALADFSFTATLPPLIVSMANGKMPGPFCKLHIYVDINLFGSVPLIGFIA 120
Db 61 TICYLNLALADFSFTATLPPLIVSMANGKMPGPFCKLHIYVDINLFGSVPLIGFIA 120
Qy 121 LDRICICVLHPVMAQNHRVTSIAKVIIVGPWILAVLTPVPLFTVTITPNGDYCTCFNF 180
Db 121 LDRICICVLHPVMAQNHRVTSIAKVIIVGPWILAVLTPVPLFTVTITPNGDYCTCFNF 180
Qy 181 ASWGTPEERBLKVAITMLTARGIIRFVIGFSLPMSIYACGLIAAKIHKKMKISSRPL 240
Db 181 ASWGTPEERBLKVAITMLTARGIIRFVIGFSLPMSIYACGLIAAKIHKKMKISSRPL 240
Qy 241 RVLTAVVASFFICWPFQVALLGTWVKEMLFYGYKKIIDILVNPTSSIAFNSCLNPM 300
Db 241 RVLTAVVASFFICWPFQVALLGTWVKEMLFYGYKKIIDILVNPTSSIAFNSCLNPM 300

Qy 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPAPTNDTAANSASPAETELQAM 351
Db 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPAPTNDTAANSASPAETELQAM 351

RESULT 9

US-10-517-956-12
; Sequence 12, Application US/10517956
; Publication No. US20050233326A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Novel Screening Method
; FILE REFERENCE: 3067WOOP
; CURRENT APPLICATION NUMBER: US/10/517, 956
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: JP 2002-173798
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: JP 2002-205470
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 12
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Mouse
US-10-517-956-12

Query Match 78.2%; Score 1420; DB 5; Length 351;

Best Local Similarity 76.3%; Pred. No. 4.9e-114;

Matches 267; Conservative 33; Mismatches 50; Indels 0; Gaps 0;

Qy 1 METNFTPLMBEVSYESAGYTVLRILPLVLGVTFVLGVLGNGLVIVWAGFRMRTVT 60
Db 1 MESNVSIHNGSEVVVYDDSTISRVLMIISMVVVSITFFLGVLGNGLVIVWAGFRMRTVT 60
Qy 61 TICYLNLALADFSFTATLPPLIVSMANGKMPGPFCKLHIYVDINLFGSVPLIGFIA 120
Db 61 TICYLNLALADFSFTATLPPLIVSMANGKMPGPFCKLHIYVDINLFGSVPLIGFIA 120
Qy 121 LDRICICVLHPVMAQNHRVTSIAKVIIVGPWILAVLTPVPLFTVTITPNGDYCTCFNF 180
Db 121 LDRICICVLHPVMAQNHRVTSIAKVIIVGPWILAVLTPVPLFTVTITPNGDYCTCFNF 180
Qy 181 ASWGTPEERBLKVAITMLTARGIIRFVIGFSLPMSIYACGLIAAKIHKKMKISSRPL 240
Db 181 ASWGTPEERBLKVAITMLTARGIIRFVIGFSLPMSIYACGLIAAKIHKKMKISSRPL 240
Qy 241 RVLTAVVASFFICWPFQVALLGTWVKEMLFYGYKKIIDILVNPTSSIAFNSCLNPM 300
Db 241 RVLTAVVASFFICWPFQVALLGTWVKEMLFYGYKKIIDILVNPTSSIAFNSCLNPM 300
Qy 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPAPTNDTAANSASPAETELQAM 350
Db 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPAPTNDTAANSASPAETELQAM 350

RESULT 10

US-10-517-956-10
; Sequence 10, Application US/10517956
; Publication No. US20050233326A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Novel Screening Method
; FILE REFERENCE: 3067WOOP
; CURRENT APPLICATION NUMBER: US/10/517, 956
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: JP 2002-173798
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: JP 2002-205470
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 10
; LENGTH: 351


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; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: Patent version 3.1
; SEQ ID NO 218
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-218

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Best Local Similarity 71.7%; Score 1318; DB 4; Length 353;
Pred. No. 3,1e-105;
Matches 253; Conservative 39; Mismatches 59; Indels 2; Gaps 1;

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DB 1 METNFSIPLNTEBEVLPPEAGHTVLMIFSILVHGTVFVGLGNGLVTVWAGFRMTRTVN 60
QY 61 TICYLNLALADSFATLPLPLVSNMAGEKMPFGWFLCKLHIIVDINLFGSVPLIGFA 120
DB 61 TICYLNLALADSFATLPLPLVSNMAGEKMPFGWFLCKLHIIVDINLFGSVPLIGFA 120
QY 121 LDRICVLHPVMAQNHRVSLAMKVIQVPMIALVLTLPVPLFTVTTIPNGDYCTENF 180
DB 121 LDRICVLHPVMAQNHRVSLAMKVIQVPMIALVLTLPVPLFTVTTIPNGDYCTENF 180
QY 181 ASNGCPPEERLKVATITMLTARGIIRFVIGFSLPMSIVACGLIAKHKKGMKSSRPL 240
DB 181 AFMGDTAVERLNVFTIMAKVFLIHPITIGFTVPMISITVCGIIAKHHRNMKSSRPL 240
QY 241 RVLTAVASFFICWPPFQVALLGTVMLEKMLFYKXKIIDLVNPTSLAFNSCLNPM 300
DB 241 RVPAVAVASFFICWPPFELIGILMAVWLKEMLNKXKIIDLVNPTSLAFNSCLNPM 300
QY 301 LVYFVGODFERRLIHSILPISLERALSE--DSAPNTDPAANSASPATTELQAM 351
DB 301 LVYFVGMRNFERIRLSIPTSLERALTVEPDSQTSNHTTSASPRETELQAM 353

RESULT 14
US-10-789-241-12
; Sequence 12, Application US/10789241
; Publication No. US20040180332A1
; GENERAL INFORMATION:
; APPLICANT: Powell, Douglas M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS USING 9145, 1725, 311, 837,
; TITLE OF INVENTION: 58305, 156, 14175, 50352, 32678, 5560, 7240, 8865, 12396,
; TITLE OF INVENTION: 12397, 13644, 19938, 2077, 1735, 1786, 10220, 17822, 33945,
; TITLE OF INVENTION: 43748, 47161, 81982 OR 46777
; FILE REFERENCE: MPIO3-041PTRNOMNIM
; CURRENT APPLICATION NUMBER: US/10/789,241
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/454,202
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/456,326
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/465,240
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 60/475,233
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 60/478,952
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/487,836
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: US 60/500,111
; PRIOR FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 53
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; SOFTWARE: FaestSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-241-12

Query Match
Best Local Similarity 72.5%; Score 1318; DB 4; Length 353;
Pred. No. 3,1e-105;
Matches 253; Conservative 39; Mismatches 59; Indels 2; Gaps 1;

QY 1 METNFTPLNEXEYBSYSSAGYTVLRILPLVVLGTVFVLGNGLVTVWAGFRMTRTYT 60
DB 1 METNFSIPLNTEBEVLPPEAGHTVLMIFSILVHGTVFVGLGNGLVTVWAGFRMTRTVN 60
QY 61 TICYLNLALADSFATLPLPLVSNMAGEKMPFGWFLCKLHIIVDINLFGSVPLIGFA 120
DB 61 TICYLNLALADSFATLPLPLVSNMAGEKMPFGWFLCKLHIIVDINLFGSVPLIGFA 120
QY 121 LDRICVLHPVMAQNHRVSLAMKVIQVPMIALVLTLPVPLFTVTTIPNGDYCTENF 180
DB 121 LDRICVLHPVMAQNHRVSLAMKVIQVPMIALVLTLPVPLFTVTTIPNGDYCTENF 180
QY 181 ASNGCPPEERLKVATITMLTARGIIRFVIGFSLPMSIVACGLIAKHKKGMKSSRPL 240
DB 181 AFMGDTAVERLNVFTIMAKVFLIHPITIGFTVPMISITVCGIIAKHHRNMKSSRPL 240
QY 241 RVLTAVASFFICWPPFQVALLGTVMLEKMLFYKXKIIDLVNPTSLAFNSCLNPM 300
DB 241 RVPAVAVASFFICWPPFELIGILMAVWLKEMLNKXKIIDLVNPTSLAFNSCLNPM 300
QY 301 LVYFVGODFERRLIHSILPISLERALSE--DSAPNTDPAANSASPATTELQAM 351
DB 301 LVYFVGMRNFERIRLSIPTSLERALTVEPDSQTSNHTTSASPRETELQAM 353

RESULT 15
US-10-517-956-14
; Sequence 14, Application US/10517956
; Publication No. US2005023326A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Novel Screening Method
; FILE REFERENCE: 3067WOOP
; CURRENT APPLICATION NUMBER: US/10/517,956
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: JP 2002-173798
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: JP 2002-205470
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 14
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Human
US-10-517-956-14

Query Match
Best Local Similarity 72.5%; Score 1318; DB 5; Length 353;
Pred. No. 3,1e-105;
Matches 253; Conservative 39; Mismatches 59; Indels 2; Gaps 1;

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DB 1 METNFSIPLNTEBEVLPPEAGHTVLMIFSILVHGTVFVGLGNGLVTVWAGFRMTRTVN 60
QY 61 TICYLNLALADSFATLPLPLVSNMAGEKMPFGWFLCKLHIIVDINLFGSVPLIGFA 120
DB 61 TICYLNLALADSFATLPLPLVSNMAGEKMPFGWFLCKLHIIVDINLFGSVPLIGFA 120
QY 121 LDRICVLHPVMAQNHRVSLAMKVIQVPMIALVLTLPVPLFTVTTIPNGDYCTENF 180
DB 121 LDRICVLHPVMAQNHRVSLAMKVIQVPMIALVLTLPVPLFTVTTIPNGDYCTENF 180
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356.787 Million cell updates/sec

Title: US-10-517-956-1
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Gapop 10.0 , Gapect 0.5

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1817	100.0	351	US-11-218-281-24	Sequence 24, App1
3	1327	73.0	353	US-11-218-281-25	Sequence 25, App1
4	1318	72.5	353	US-10-508-765-2	Sequence 2, App1
5	1243.5	68.4	350	US-11-218-281-23	Sequence 23, App1
6	553.5	30.5	356	US-11-218-281-27	Sequence 27, App1
7	538.5	29.6	371	US-11-134-811-4	Sequence 4, App1
8	538.5	29.6	371	US-11-218-281-2	Sequence 2, App1
9	538.5	29.6	371	US-11-218-281-33	Sequence 33, App1
10	534.5	29.4	373	US-11-134-811-2	Sequence 2, App1
11	534.5	29.4	373	US-11-218-281-1	Sequence 1, App1
12	534.5	29.4	373	US-11-218-281-28	Sequence 28, App1
13	513	28.2	350	US-10-502-145-1	Sequence 1, App1
14	513	28.2	350	US-11-169-976-9	Sequence 9, App1
15	513	28.2	350	US-11-218-281-31	Sequence 31, App1
16	509.5	28.0	482	US-11-218-281-30	Sequence 30, App1
17	508.5	28.0	482	US-11-169-976-2	Sequence 2, App1
18	504.5	27.8	355	US-11-218-281-29	Sequence 29, App1
19	502.5	27.7	371	US-11-134-811-6	Sequence 6, App1
20	502.5	27.7	371	US-11-218-281-1	Sequence 1, App1
21	499	27.5	355	US-11-218-281-26	Sequence 26, App1
22	426.5	23.5	359	US-11-017-058-9	Sequence 9, App1
23	426.5	23.5	359	US-10-995-561-712	Sequence 712, App1
24	426.5	23.5	359	US-10-995-561-716	Sequence 716, App1
25	426.5	23.5	359	US-11-127-877-65	Sequence 65, App1

26	426.5	23.5	388	6	US-10-995-561-713	Sequence 713, App
27	426.5	23.5	388	6	US-10-995-561-714	Sequence 714, App
28	426.5	23.5	394	6	US-10-995-561-715	Sequence 715, App
29	423.5	23.3	359	6	US-10-876-787-2	Sequence 2, App1
30	419.5	23.1	352	7	US-11-028-922A-1	Sequence 1, App1
31	417.5	23.0	349	7	US-11-028-922A-2	Sequence 2, App1
32	399.5	22.0	350	7	US-11-249-847-546	Sequence 546, App
33	393	21.6	400	7	US-11-127-877-55	Sequence 55, App1
34	386.5	21.3	348	6	US-10-330-773-921	Sequence 921, App
35	382.5	21.1	388	6	US-10-995-561-838	Sequence 838, App
36	382.5	21.1	389	6	US-10-995-561-837	Sequence 837, App
37	380.5	20.9	357	7	US-11-261-135-2	Sequence 2, App1
38	380	20.9	355	6	US-10-330-773-918	Sequence 918, App
39	370	20.4	367	6	US-10-920-055-7	Sequence 7, App1
40	366.5	20.2	337	6	US-10-980-388-115	Sequence 115, App
41	366	20.1	254	6	US-10-055-877-327	Sequence 327, App
42	366	20.1	254	6	US-10-055-877-327	Sequence 327, App
43	366	20.1	254	6	US-10-055-877-340	Sequence 340, App
44	366	20.1	254	6	US-10-877-346-83	Sequence 83, App1
45	362.5	20.0	259	6	US-10-055-877-225	Sequence 225, App1

ALIGNMENTS

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RESULT 1
US-11-218-281-12
; Sequence 12, Application US//11218281
; Publication NO. US20060024758A1
; GENERAL INFORMATION:
; APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
; APPLICANT: Serhan, Charles N.
; APPLICANT: Arica, Makoto
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
; TITLE OF INVENTION: RECEPTORS FOR EICOSAPENTAENOIC ACID ANALOGS
; FILE REFERENCE: MP-14448-05
; CURRENT APPLICATION NUMBER: US/11/218, 281
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: 60/452, 244
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 351
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-11-218-281-12

Query Match      100.0%; Score 1817; DB 7; Length 351;
Best Local Similarity 100.0%; Pred. No. 2,1e-136;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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        |||
DB      1 METNFSPTPLNREYEVSEAGYVLAIRLPLVVLGTFVGLGNGVIVWAGFRMRTYV 60

QY      61 TICCYMALADPSFTATLPLFLISVAMGKMPGFLCQIHIVVDINFGSVFLGFLA 120
        |||
DB      61 TICCYMALADPSFTATLPLFLISVAMGKMPGFLCQIHIVVDINFGSVFLGFLA 120

QY      121 LDRICVLPVPAQNRTVSLAMKVIWGPWIALVTLTPVFLITVTIPNGDYCTFNF 180
        |||
DB      121 LDRICVLPVPAQNRTVSLAMKVIWGPWIALVTLTPVFLITVTIPNGDYCTFNF 180

QY      181 ASWGTPEERLKAITMTLARGIRIVIFPSLPMSVACYGLIAKHKKGKITSRPL 240
        |||
DB      181 ASWGTPEERLKAITMTLARGIRIVIFPSLPMSVACYGLIAKHKKGKITSRPL 240

QY      241 RVLTAVASFFICFPFQVALAGTVMLEKMLFYGKXKIIDILVNPTSSLAFFNSCLNPM 300
        |||
DB      241 RVLTAVASFFICFPFQVALAGTVMLEKMLFYGKXKIIDILVNPTSSLAFFNSCLNPM 300

QY      301 LVYFGQDFRRLIHSLPTSLERALSDESAPTNDTAANSAPPAETELQAM 351
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Db 301 LVFVGGDFRRLIHSLSPTSLERALSBDSPATNDTAAANSPPAELELOQM 351

RESULT 2
US-11-218-281-24
Sequence 24, Application US/11218281
Publication No. US20060024758A1

GENERAL INFORMATION:
APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
APPLICANT: Serhan, Charles N.

APPLICANT: Arica, Makoto
TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
FILE REFERENCE: MP-14448.05
CURRENT APPLICATION NUMBER: US/11/218,281

CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: 60/452,244
PRIOR FILING DATE: 2003-03-05

NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24

LENGTH: 351
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-11-218-281-24

Query Match 100.0%; Score 1817; DB 7; Length 351;
Best Local Similarity 100.0%; Pred. No. 2,1e-136;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TICYLNLALADSFPTATLPFLIVSMAMGKMPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120
DB 61 TICYLNLALADSFPTATLPFLIVSMAMGKMPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120

QY 121 LDRICIVLHPVMAQNHRVTSIAKVIIVGPWILAVLTPVFLTTVTIIPNGDTYCTFNF 180
DB 121 LDRICIVLHPVMAQNHRVTSIAKVIIVGPWILAVLTPVFLTTVTIIPNGDTYCTFNF 180

QY 181 ASWGTPEERLKVATIMLTARGIIRFVIGSLPMSIVAICYGLIAKIHKGMIKSSRPL 240
DB 181 ASWGTPEERLKVATIMLTARGIIRFVIGSLPMSIVAICYGLIAKIHKGMIKSSRPL 240

QY 241 RVLTAVASFFICWPPQVALGTVWLKEMLFYGYKXIIDLVPNTSSLAFFNSCLNPM 300
DB 241 RVLTAVASFFICWPPQVALGTVWLKEMLFYGYKXIIDLVPNTSSLAFFNSCLNPM 300

QY 301 LVFVGGDFRRLIHSLSPTSLERALSBDSPATNDTAAANSPPAELELOQM 351
DB 301 LVFVGGDFRRLIHSLSPTSLERALSBDSPATNDTAAANSPPAELELOQM 351

RESULT 3
US-11-218-281-25
Sequence 25, Application US/11218281
Publication No. US20060024758A1

GENERAL INFORMATION:
APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
APPLICANT: Serhan, Charles N.

APPLICANT: Arica, Makoto
TITLE OF INVENTION: RECEPTORS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
FILE REFERENCE: MP-14448.05
CURRENT APPLICATION NUMBER: US/11/218,281

CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: 60/452,244
PRIOR FILING DATE: 2003-03-05

NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.2

; SEQ ID NO 25
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-11-218-281-25

Query Match 73.0%; Score 1327; DB 7; Length 353;
Best Local Similarity 72.2%; Pred. No. 1e-97;
Matches 255; Conservative 38; Mismatches 58; Indels 2; Gaps 1;

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QY 61 TICYLNLALADSFPTATLPFLIVSMAMGKMPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120
DB 61 TICYLNLALADSFPTATLPFLIVSMAMGKMPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120

QY 121 LDRICIVLHPVMAQNHRVTSIAKVIIVGPWILAVLTPVFLTTVTIIPNGDTYCTFNF 180
DB 121 LDRICIVLHPVMAQNHRVTSIAKVIIVGPWILAVLTPVFLTTVTIIPNGDTYCTFNF 180

QY 181 ASWGTPEERLKVATIMLTARGIIRFVIGSLPMSIVAICYGLIAKIHKGMIKSSRPL 240
DB 181 ASWGTPEERLKVATIMLTARGIIRFVIGSLPMSIVAICYGLIAKIHKGMIKSSRPL 240

QY 241 RVLTAVASFFICWPPQVALGTVWLKEMLFYGYKXIIDLVPNTSSLAFFNSCLNPM 300
DB 241 RVLTAVASFFICWPPQVALGTVWLKEMLFYGYKXIIDLVPNTSSLAFFNSCLNPM 300

QY 301 LVFVGGDFRRLIHSLSPTSLERALSBDSPATNDTAAANSPPAELELOQM 351
DB 301 LVFVGGDFRRLIHSLSPTSLERALSBDSPATNDTAAANSPPAELELOQM 351

RESULT 4
US-10-508-765-2
Sequence 2, Application US/10508765
Publication No. US20060057577A1

GENERAL INFORMATION:
APPLICANT: Goetz, Stefan
APPLICANT: Bruggemeier, Ulf

APPLICANT: Goetz, Andreas
TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with Homo
FILE REFERENCE: Le A 35 838
CURRENT APPLICATION NUMBER: US/10/508,765

CURRENT FILING DATE: 2004-09-22
PRIOR APPLICATION NUMBER: PCT/EP03/02414
PRIOR FILING DATE: 2003-03-10

PRIOR APPLICATION NUMBER: EP 02006595.9
PRIOR FILING DATE: 2002-03-22
NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn version 3.3
SEQ ID NO 2
LENGTH: 353
TYPE: PRT
ORGANISM: Homo sapiens
US-10-508-765-2

Query Match 72.5%; Score 1318; DB 6; Length 353;
Best Local Similarity 71.7%; Pred. No. 5.2e-97;
Matches 253; Conservative 39; Mismatches 59; Indels 2; Gaps 1;

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DB 1 METNSTPLANEYEBVSYSAGYTVLRILPLVVLGTVFVLGNGLVIVVAGFRMTRTYT 60

QY 61 TICYLNLALADSFPTATLPFLIVSMAMGKMPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120
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RESULT 5 US-11-218-281-23

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; Sequence 23, Application US/11218281
; Publication No. US20060024758A1
; GENERAL INFORMATION:
; APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
; APPLICANT: Serhan, Charles N.
; APPLICANT: Arita, Makoto
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
; FILE REFERENCE: MP-14448-05
; CURRENT APPLICATION NUMBER: US/11/218, 281
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: 60/452,244
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 350
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-11-218-281-23

```

```

Query Match      68.4%; Score 1243.5; DB 7; Length 350;
Best Local Similarity 68.6%; Pred. No. 3,9e-91;
Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps 1;

```

```

Qy      1 METNFSPTLAEYEVSEYAGYTVLRIPLVLGVTVLGVNGVIVVAGFPMRTVT 60
Db      1 METNFSPTLAEYEVSEYAGYTVLRIPLVLGVTVLGVNGVIVVAGFPMRTVT 60
Qy      61 TICVNLALADFSFTATLPLIVSMANGKMPFGMLCKLIHIVVDINLFGSVFLIGFIA 120
Db      61 TICVNLALADFSFTATLPLIVSMANGKMPFGMLCKLIHIVVDINLFGSVFLIGFIA 120
Qy      121 LDRICLHHPMAQNHMTSLAKRWMTGLWIFITVLPLPFMTITSTNGTYCIENF 180
Db      121 LDRICLHHPMAQNHMTSLAKRWMTGLWIFITVLPLPFMTITSTNGTYCIENF 180
Qy      181 ASNGGTPEERLKAITMTLARGIIRFVIGSLPMSIYACGLIAKHKKMKSSRPL 240
Db      181 ASNGGTPEERLKAITMTLARGIIRFVIGSLPMSIYACGLIAKHKKMKSSRPL 240
Qy      241 RVLTAIVASFFICMPFQOLVALGTVWLKEMLFYKXKIIDIIVNPTSSLAFFNSCLNPM 300
Db      241 RVLTAIVASFFICMPFQOLVALGTVWLKEMLFYKXKIIDIIVNPTSSLAFFNSCLNPM 300
Qy      301 LYFVGGDFEERLIHSLPTSLERALS--DSAPNDTAAASAPPAETELQAM 350
Db      301 LYFVGGDFEERLIHSLPTSLERALS--DSAPNDTAAASAPPAETELQAM 350

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RESULT 6
US-11-218-281-27
; Sequence 27, Application US/11218281
; Publication No. US20060024758A1
; GENERAL INFORMATION:

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```

; APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
; APPLICANT: Serhan, Charles N.
; APPLICANT: Arita, Makoto
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
; FILE REFERENCE: MP-14448-05
; CURRENT APPLICATION NUMBER: US/11/218, 281
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: 60/452,244
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 356
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-11-218-281-27

```

```

Query Match      30.5%; Score 553.5; DB 7; Length 356;
Best Local Similarity 41.0%; Pred. No. 1.2e-36;
Matches 126; Conservative 59; Mismatches 113; Indels 9; Gaps 4;

```

```

Qy      25 LRIPLVLGVTVLGVNGVIVVAGFPMRTVTITCYLNLALADFSFTATLP--PL 81
Db      42 LRIPLVLGVTVLGVNGVIVVAGFPMRTVTITCYLNLALADFSFTATLP--PL 101
Qy      82 IVSMANGKMPFGMLCKLIHIVVDINLFGSVFLIGFIALDRICLHHPMAQNHMTSL 141
Db      102 IVS---RQMLGEMAKKIYIFVFLSYFASNLVIFISVDCISVLYPMVNLNHTVOR 157
Qy      142 AMKVIVGPMILALVTLVPFLFTTYTINNGDTYCTCFNPAKSGTPEERLKAITMTAR 201
Db      158 ASWLAGVWLAAALCSAHLKFTTRKW--NGCTHCYLAARNSDETQIWEVGEHIIIG 216
Qy      202 GILRFVIGSLPMSIYACGLIAKHKKMKSSRPLRVLTAIVASFFICMPFQOLVA 261
Db      217 TIGHFLGFLGPIALITGCHLRAKDLRGVHAKPRKLLVLSAFLIPFSPRNV- 275
Qy      262 LIGTVWLKEMLFYKXKIIDIIVNPTSSLAFFNSCLNPMLYVVGDFEERLIHSLPTSL 321
Db      276 LVLHMKRRVWLKEIYHPRMLILIQASFALGCVNSSLNPLVYVVGDFEERLIHSLPTSL 335
Qy      322 ERALSED 328
Db      336 ARAFGEE 342

```

```

RESULT 7
US-11-134-811-4
; Sequence 4, Application US/11134811
; Publication No. US20060024750A1
; GENERAL INFORMATION:
; APPLICANT: Wiltamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandebogaerde, Ann
; APPLICANT: Decheux, Michel
; APPLICANT: Parentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerin
; FILE REFERENCE: 9409/2043
; CURRENT APPLICATION NUMBER: US/11/134, 811
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: PCT/EP02/07647
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 4
; LENGTH: 371
; TYPE: PRN
; ORGANISM: Mus musculus
US-11-134-811-4

```

```

Query Match      29.6%; Score 538.5; DB 7; Length 371;
Best Local Similarity 35.2%; Pred. No. 1.9e-35;
Matches 120; Conservative 70; Mismatches 124; Indels 27; Gaps 8;

```

```

QY 10 NEYEE-----VSYESAGYTVLRILP---LVVLGVTFVLGNGLVYVWAGFMRTRVTT 61
DB 14 DEYSDEGFGYVDEEASPEAKAVAPFLVIVYISLVCFGLGNGLVIVATFPMKKTIVNT 73
QY 62 ICYNLALADFSFTATLPFLIVSMANGKMPFGMFLCKLIHIVDINLFGSVFLIGFIAL 121
DB 74 VWFVNLAADVDFLNFILPMMITTAADYHNVFGKAMCKISNFLSHNMVTSVFLTLVTSF 133
QY 122 DRICIVLHPVMAONHRTVSLAMKVIYGPWILALVTLVPLVFLTYTTPNGDTYCTFNPA 181
DB 134 DRICIVLHPVMSQNHRSIRLAIVMTCSAVWVLAFLSPSLVFRDTANI-HGKITCFNNFS 192
QY 182 SWGCTPEERLKAIVMLTARG-----IIRFVIGSLPMGIVAI CYGLIAKHKKGM 233
DB 193 L--AADESSPHRHSQVSTGYSRHVAATVTRFLCGFLVFLITACVLTTFVKLQNRRL 250
QY 234 IKSRRLRLVLTAVASFFICWPFQVALLGTWMLKEMLFYGYKIIDILVNP-TSSLAF 292
DB 251 ANKKKPFKIIITITITFLCWCPRH-----TLVLELHHTRAVPSVSGLPLATAVAI 304
QY 293 FNSCLNPMILYFVGODFRERLIHSLPTSLERALSDESAPTN 333
DB 305 ANSCNMPILYVFMGHDPRFKFV-ALFSRLANLALSDTGPSS 344

```

```

RESULT 8
US-11-218-281-2
; Sequence 2, Application US/11218281
; Publication No. US20060024758A1
; GENERAL INFORMATION:
; APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
; APPLICANT: Serhan, Charles N.
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
; FILE REFERENCE: MP-14448.05
; CURRENT APPLICATION NUMBER: US/11/218,281
; PRIOR FILING DATE: 2005-09-01
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 371
; TYPE: PRN
; ORGANISM: MOUSE
US-11-218-281-2

```

```

Query Match      29.6%; Score 538.5; DB 7; Length 371;
Best Local Similarity 35.2%; Pred. No. 1.9e-35;
Matches 120; Conservative 70; Mismatches 124; Indels 27; Gaps 8;

```

```

QY 10 NEYEE-----VSYESAGYTVLRILP---LVVLGVTFVLGNGLVYVWAGFMRTRVTT 61
DB 14 DEYSDEGFGYVDEEASPEAKAVAPFLVIVYISLVCFGLGNGLVIVATFPMKKTIVNT 73
QY 62 ICYNLALADFSFTATLPFLIVSMANGKMPFGMFLCKLIHIVDINLFGSVFLIGFIAL 121
DB 74 VWFVNLAADVDFLNFILPMMITTAADYHNVFGKAMCKISNFLSHNMVTSVFLTLVTSF 133
QY 122 DRICIVLHPVMAONHRTVSLAMKVIYGPWILALVTLVPLVFLTYTTPNGDTYCTFNPA 181
DB 134 DRICIVLHPVMSQNHRSIRLAIVMTCSAVWVLAFLSPSLVFRDTANI-HGKITCFNNFS 192

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```

QY 182 SWGCTPEERLKAIVMLTARG-----IIRFVIGSLPMGIVAI CYGLIAKHKKGM 233
DB 193 L--AADESSPHRHSQVSTGYSRHVAATVTRFLCGFLVFLITACVLTTFVKLQNRRL 250
QY 234 IKSRRLRLVLTAVASFFICWPFQVALLGTWMLKEMLFYGYKIIDILVNP-TSSLAF 292
DB 251 ANKKKPFKIIITITITFLCWCPRH-----TLVLELHHTRAVPSVSGLPLATAVAI 304
QY 293 FNSCLNPMILYFVGODFRERLIHSLPTSLERALSDESAPTN 333
DB 305 ANSCNMPILYVFMGHDPRFKFV-ALFSRLANLALSDTGPSS 344

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```

RESULT 9
US-11-218-281-33
; Sequence 33, Application US/11218281
; Publication No. US20060024758A1
; GENERAL INFORMATION:
; APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
; APPLICANT: Serhan, Charles N.
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
; FILE REFERENCE: MP-14448.05
; CURRENT APPLICATION NUMBER: US/11/218,281
; PRIOR FILING DATE: 2005-09-01
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 371
; TYPE: PRN
; ORGANISM: MOUSE
US-11-218-281-33

```

```

Query Match      29.6%; Score 538.5; DB 7; Length 371;
Best Local Similarity 35.2%; Pred. No. 1.9e-35;
Matches 120; Conservative 70; Mismatches 124; Indels 27; Gaps 8;

```

```

QY 10 NEYEE-----VSYESAGYTVLRILP---LVVLGVTFVLGNGLVYVWAGFMRTRVTT 61
DB 14 DEYSDEGFGYVDEEASPEAKAVAPFLVIVYISLVCFGLGNGLVIVATFPMKKTIVNT 73
QY 62 ICYNLALADFSFTATLPFLIVSMANGKMPFGMFLCKLIHIVDINLFGSVFLIGFIAL 121
DB 74 VWFVNLAADVDFLNFILPMMITTAADYHNVFGKAMCKISNFLSHNMVTSVFLTLVTSF 133
QY 122 DRICIVLHPVMAONHRTVSLAMKVIYGPWILALVTLVPLVFLTYTTPNGDTYCTFNPA 181
DB 134 DRICIVLHPVMSQNHRSIRLAIVMTCSAVWVLAFLSPSLVFRDTANI-HGKITCFNNFS 192
QY 182 SWGCTPEERLKAIVMLTARG-----IIRFVIGSLPMGIVAI CYGLIAKHKKGM 233
DB 193 L--AADESSPHRHSQVSTGYSRHVAATVTRFLCGFLVFLITACVLTTFVKLQNRRL 250
QY 234 IKSRRLRLVLTAVASFFICWPFQVALLGTWMLKEMLFYGYKIIDILVNP-TSSLAF 292
DB 251 ANKKKPFKIIITITITFLCWCPRH-----TLVLELHHTRAVPSVSGLPLATAVAI 304
QY 293 FNSCLNPMILYFVGODFRERLIHSLPTSLERALSDESAPTN 333
DB 305 ANSCNMPILYVFMGHDPRFKFV-ALFSRLANLALSDTGPSS 344

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```

RESULT 10
US-11-134-811-2
; Sequence 2, Application US/11134811
; Publication No. US20060024750A1
; GENERAL INFORMATION:
; APPLICANT: Wiltamier, Valerie
; APPLICANT: Commun1, David

```

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; APPLICANT: Vandenberg, Ann
; APPLICANT: Decheux, Michel
; APPLICANT: Parentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerin
; FILE REFERENCE: 9409/2003
; CURRENT APPLICATION NUMBER: US/11/134,811
; PRIOR FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: PCT/EP02/07647
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-811-2

Query Match
Best Local Similarity 29.4%; Score 534.5; DB 7; Length 371;
Pred. No. 3.9e-35;
Matches 122; Conservative 65; Mismatches 130; Indels 19; Gaps 7;

QY 24 VRIILPLVVLGVTVFVGLVGLVGLVIVVAGFRMTRTVTTCYLNALADSFATLPLFLIV 83
DB 36 VTRIFLVVYSIVCFGLIGLNGLVIIATFKKKKTVNMWVPLNLAADFLFVNFPLIHIT 95

QY 84 SNAMGEKMPGWFCLCKLHIIVNDINLFGSVFLIGFALDRICICVLPVWQNHRTYSLAM 143
DB 96 YAMADYHWVFGTAMCKISNPLIHNMTSVFLITLTISSDRICISVLLPVWSQNHRSVRLAY 155

QY 144 KVIYGPMTALVLTLPVFLFTVTTPNGDTYCTNF-----ASWGTPEBRLLKVAIT 196
DB 156 MACMTVWLAFLFSSPSLVFRDPAHL-HGKISCNNFSLSTGSSSW-PTHSQMDPVGIS 213

QY 197 MLTARGIIRFVIGFSLPMSIVAICYGLIAKIKKGMKISSRPLRLVLTAVASFFICWPP 256
DB 214 RHVVTVTRFLGFLVPLVLTITACVLTIVCKLQRRLAKTKKPKFIIVTIIITFLCWCP 273

QY 257 FQVALLGTWVKEMLFYGKYKIIDLVNPTSSLAFLNSCLNPLIYFVGQDFRRLIHS 316
DB 274 YHTLNLLE---LHHTAMPG--SVFSIGLPLATLAIANSQNPILYVFMGDFKKKCV-A 327

QY 317 LPTSLERLSED-----SAPTNDTAANSAPPAETEL 348
DB 328 LFSRLVNALSEDTGHSSYPSHRSFTKMSMNERTISM 363

RESULT 11
US-11-218-281-1
; Sequence 1, Application US/11218281
; Publication No. US20060024758A1
; GENERAL INFORMATION:
; APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
; APPLICANT: Artea, Makoto
; TITLE OF INVENTION: RECEPTORS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
; FILE REFERENCE: MP-14448.05
; CURRENT APPLICATION NUMBER: US/11/218,281
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: 60/452,244
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 373

```

```

; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-11-218-281-1

Query Match
Best Local Similarity 29.4%; Score 534.5; DB 7; Length 373;
Pred. No. 3.9e-35;
Matches 122; Conservative 65; Mismatches 130; Indels 19; Gaps 7;

QY 24 VRIILPLVVLGVTVFVGLVGLVGLVIVVAGFRMTRTVTTCYLNALADSFATLPLFLIV 83
DB 36 VTRIFLVVYSIVCFGLIGLNGLVIIATFKKKKTVNMWVPLNLAADFLFVNFPLIHIT 97

QY 84 SNAMGEKMPGWFCLCKLHIIVNDINLFGSVFLIGFALDRICICVLPVWQNHRTYSLAM 143
DB 96 YAMADYHWVFGTAMCKISNPLIHNMTSVFLITLTISSDRICISVLLPVWSQNHRSVRLAY 157

QY 144 KVIYGPMTALVLTLPVFLFTVTTPNGDTYCTNF-----ASWGTPEBRLLKVAIT 196
DB 156 MACMTVWLAFLFSSPSLVFRDPAHL-HGKISCNNFSLSTGSSSW-PTHSQMDPVGIS 215

QY 197 MLTARGIIRFVIGFSLPMSIVAICYGLIAKIKKGMKISSRPLRLVLTAVASFFICWPP 256
DB 216 RHVVTVTRFLGFLVPLVLTITACVLTIVCKLQRRLAKTKKPKFIIVTIIITFLCWCP 275

QY 257 FQVALLGTWVKEMLFYGKYKIIDLVNPTSSLAFLNSCLNPLIYFVGQDFRRLIHS 316
DB 276 YHTLNLLE---LHHTAMPG--SVFSIGLPLATLAIANSQNPILYVFMGDFKKKCV-A 329

QY 317 LPTSLERLSED-----SAPTNDTAANSAPPAETEL 348
DB 330 LFSRLVNALSEDTGHSSYPSHRSFTKMSMNERTISM 365

RESULT 12
US-11-218-281-28
; Sequence 28, Application US/11218281
; Publication No. US20060024758A1
; GENERAL INFORMATION:
; APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
; APPLICANT: Artea, Makoto
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
; FILE REFERENCE: MP-14448.05
; CURRENT APPLICATION NUMBER: US/11/218,281
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: 60/452,244
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 373
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-11-218-281-28

Query Match
Best Local Similarity 29.4%; Score 534.5; DB 7; Length 373;
Pred. No. 3.9e-35;
Matches 122; Conservative 65; Mismatches 130; Indels 19; Gaps 7;

QY 24 VRIILPLVVLGVTVFVGLVGLVGLVIVVAGFRMTRTVTTCYLNALADSFATLPLFLIV 83
DB 38 VTRIFLVVYSIVCFGLIGLNGLVIIATFKKKKTVNMWVPLNLAADFLFVNFPLIHIT 97

QY 84 SNAMGEKMPGWFCLCKLHIIVNDINLFGSVFLIGFALDRICICVLPVWQNHRTYSLAM 143
DB 98 YAMADYHWVFGTAMCKISNPLIHNMTSVFLITLTISSDRICISVLLPVWSQNHRSVRLAY 157

QY 144 KVIYGPMTALVLTLPVFLFTVTTPNGDTYCTNF-----ASWGTPEBRLLKVAIT 196
DB 158 MACMTVWLAFLFSSPSLVFRDPAHL-HGKISCNNFSLSTGSSSW-PTHSQMDPVGIS 215

QY 197 MLTARGIIRFVIGFSLPMSIVAICYGLIAKIKKGMKISSRPLRLVLTAVASFFICWPP 256

```

```
Db 216 RHVVVTRRLCGELVFLVLTITACVLTIVCKLQGRNLRKPKPKKIIVTIIIFFLCMCP 275
Qy 257 FQVALLIGTWLKEMLFYGKKIIDIIVNPTSLAFNSCLNPMLVYFVGQDFRERLIHS 316
Db 276 YHTLNTLLE---LHHTAMPG--SVFSLDLPALALAINSCNPIILYFMGODEFKKCV-A 329
Qy 317 LPTSLERALSSED-----SAPINDRAANSAPPAETEL 348
Db 330 LFSRLVVALSEDTGHSYPSHRSTTKNSMNERISM 365
```

RESULT 13

```
US-10-502-145-1
/ Sequence 1, Application US/10502145
/ Publication No. US2005024406A1
/ GENERAL INFORMATION:
/ APPLICANT: MACKAY, CHARLES REAY
/ TITLE OF INVENTION: Anti-C5ar antibodies and uses thereof
/ FILE REFERENCE: RICE-032
/ CURRENT APPLICATION NUMBER: US/10/502,145
/ PRIOR FILING DATE: 2004-07-19
/ PRIOR APPLICATION NUMBER: USSN 60/350,961
/ PRIOR FILING DATE: 2002-01-25
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 350
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-502-145-1
```

Query Match 28.2%; Score 513; DB 6; Length 350;
Best Local Similarity 33.6%; Pred. No. 1.8e-33;
Matches 122; Conservative 60; Mismatches 129; Indels 52; Gaps 9;

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Qy 4 NFSTP-LNEYEE-----VYESAGYTVLRILPLVVLGVTFLVGLGNGLVIVAGF 53
Db 5 NYTTPDYGHYDDKDTLDLNTPVDKTSNTLRVPDILALVFAVFLVGVGNALVWVWTA 64
Qy 54 RMTRTVTTTCYNLALADSFATILPPLIVSMAMGEKMPGWFCLKIHIIVDINLFGSV 113
Db 65 EAKRTINAIWFLNLAVADFLSCLALPILFTSIQHHHMPFGAACSILPSILILNNYASI 124
Qy 114 FLIGFIALDRICVLPVNAQNRRTVSLAMKVIQVPMILAVLTLPVFLFTVTITPNGD 173
Db 125 LILATISADRFLLVFPKIQCFRGAGLAWIACAVAMGLALLTIPSPFLRVV-----RE 179
Qy 174 TY-----CTFNPASMGTPBERLKVAILMTLARGIIRFVIGFSLPMSIVAICYGILAAK 227
Db 180 EYFPPKVLGVDYSH-----DKRRERAV-----AIVRLVGLFLWPLTLTTCYTPILR 228
Qy 228 IHKGMKISRPLRVLTAVVASFFICMPPQVALLGTWLKEMLFYGGKKIIDIIVNPT 287
Db 229 TWRBRATRSTKTLKVAVVASFFIFWLPYQVTGIM-----MSLEBSSPTFLILNK 281
Qy 288 SSL-----AFNSCLNPMLVYFVGQDFRERLIHSLPTELSERALSBSA-----PTND 334
Db 282 DSLCVSPAYINCCINPIIYVAVAGQFGRLKSLPSILRNVLTEBSVVRSEKSPTRSTVD 341
Qy 335 TAA 337
Db 342 TWA 344
```

RESULT 14

```
US-11-169-976-9
/ Sequence 9, Application US/11169976
/ Publication No. US20060014249A1
/ GENERAL INFORMATION:
/ APPLICANT: Li, et al.
/ TITLE OF INVENTION: Human G-Protein Coupled Receptor
/ FILE REFERENCE: PFI59P1C2
```

```
/ CURRENT APPLICATION NUMBER: US/11/169,976
/ PRIOR FILING DATE: 2005-06-30
/ PRIOR APPLICATION NUMBER: 10/259,521
/ PRIOR FILING DATE: 2002-09-30
/ PRIOR APPLICATION NUMBER: 08/462,314
/ PRIOR FILING DATE: 1995-06-05
/ PRIOR APPLICATION NUMBER: PCT/US95/01992
/ PRIOR FILING DATE: 1995-02-17
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 9
/ LENGTH: 350
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-11-169-976-9
```

Query Match 28.2%; Score 513; DB 7; Length 350;
Best Local Similarity 33.6%; Pred. No. 1.8e-33;
Matches 122; Conservative 60; Mismatches 129; Indels 52; Gaps 9;

```
Qy 4 NFSTP-LNEYEE-----VYESAGYTVLRILPLVVLGVTFLVGLGNGLVIVAGF 53
Db 5 NYTTPDYGHYDDKDTLDLNTPVDKTSNTLRVPDILALVFAVFLVGVGNALVWVWTA 64
Qy 54 RMTRTVTTTCYNLALADSFATILPPLIVSMAMGEKMPGWFCLKIHIIVDINLFGSV 113
Db 65 EAKRTINAIWFLNLAVADFLSCLALPILFTSIQHHHMPFGAACSILPSILILNNYASI 124
Qy 114 FLIGFIALDRICVLPVNAQNRRTVSLAMKVIQVPMILAVLTLPVFLFTVTITPNGD 173
Db 125 LILATISADRFLLVFPKIQCFRGAGLAWIACAVAMGLALLTIPSPFLRVV-----RE 179
Qy 174 TY-----CTFNPASMGTPBERLKVAILMTLARGIIRFVIGFSLPMSIVAICYGILAAK 227
Db 180 EYFPPKVLGVDYSH-----DKRRERAV-----AIVRLVGLFLWPLTLTTCYTPILR 228
Qy 228 IHKGMKISRPLRVLTAVVASFFICMPPQVALLGTWLKEMLFYGGKKIIDIIVNPT 287
Db 229 TWRBRATRSTKTLKVAVVASFFIFWLPYQVTGIM-----MSLEBSSPTFLILNK 281
Qy 288 SSL-----AFNSCLNPMLVYFVGQDFRERLIHSLPTELSERALSBSA-----PTND 334
Db 282 DSLCVSPAYINCCINPIIYVAVAGQFGRLKSLPSILRNVLTEBSVVRSEKSPTRSTVD 341
Qy 335 TAA 337
Db 342 TWA 344
```

RESULT 15

```
US-11-218-281-31
/ Sequence 31, Application US/11218281
/ Publication No. US20060024758A1
/ GENERAL INFORMATION:
/ APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
/ APPLICANT: Serhan, Charles N.
/ TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
/ TITLE OF INVENTION: RECEPTORS FOR ECOSAPENTAENOIC ACID ANALOGS
/ FILE REFERENCE: MP-14448_05
/ CURRENT APPLICATION NUMBER: US/11/218,281
/ PRIOR FILING DATE: 2005-09-01
/ PRIOR APPLICATION NUMBER: 60/452,244
/ PRIOR FILING DATE: 2003-03-05
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 31
/ LENGTH: 350
/ TYPE: PRF
/ ORGANISM: HOMO SAPIENS
US-11-218-281-31
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Query Match 28.2%; Score 513; DB 7; Length 350;

Best Local Similarity 33.6%; Pred. No. 1.8e-33;
Matches 122; Conservative 60; Mismatches 129; Indels 52; Gaps 9;

QY 4 NPSLP-LNEYE-----VSYSAGYVLRILPLVLGVTFLVGLGAVINAGF 53
Db 5 NYTTDPGVGHDDVDLDTLNTPVDKTSNTLRVDDILALIVPAVFLVGLVGNALVYVNTAF 64
QY 54 RMTRTVTTI CYLNLALADSFATLIPPLIVSNAMGEKMPFGMFLCKLIHIVDINLFGSV 113
Db 65 EAKRTINAIWPLNLAVADFLSCIALPILETSTVQHNNHPFGCAACSLIPSLIILMYASI 124
QY 114 FLIGFLALDRICIVLHPVAKONHRVLSAMKIYSPVLLAVLVLPLVPLFTTYTINGD 173
Db 125 LLATLTSIAORFLVLFVPIPCQNFREGALMTACAVAMELALLTTPSPFLYKVV-----RE 179
QY 174 TY-----CTPNASWGTPBEERLKAITMTLARGIIRFVIGFSLPSMIVACGLYIAK 227
Db 180 EYPPKVLGCVDTSH-----DKREBAV-----ATVALVGLFMPLLTITCYTFILLR 228
QY 228 IHKKGIKSRPLRLVLTAVASFPICWPFQOLVALLAGVLMKENTFYGKYIIDILVNPT 287
Db 229 TWSRRATRGTKLKVAVVAVASFFIFMLPYQTGM-----MSPLESPPTFLINKL 281
QY 288 SSG-----AFNSCLNMLYVFWGODFRERLHSLFTSIERALSEDA-----FTND 334
Db 282 DSLCSFAYAINCINPIIIVVAGOGFQGRKSLPSLIRNLVLTESVVRBSKSFSTRVD 341
QY 335 TAA 337
Db 342 TMA 344

Search completed: March 28, 2006, 13:26:39

Job time : 30.016 secs

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ORGANISM: Homo sapiens
US-10-341-434-167

Query Match 100.0%; Score 120; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPRGSCLLLTSEIDL PVKRR 24
DB 1 MAPRGSCLLLTSEIDL PVKRR 24

RESULT 3
US-10-341-434-200
Sequence 200, Application US/10341434
Publication No. US20030215835A1
GENERAL INFORMATION:

APPLICANT: Origene Technologies
TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REFERENCE: 9U 204 205 R1
CURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/348,164
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/348,119
PRIOR FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 238
SOFTWARE: PatentIn version 3.1
SEQ ID NO 200
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
US-10-341-434-200

Query Match 100.0%; Score 120; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPRGSCLLLTSEIDL PVKRR 24
DB 1 MAPRGSCLLLTSEIDL PVKRR 24

RESULT 4
US-10-716-432-1
Sequence 1, Application US/10716432
Publication No. US2005005620A1
GENERAL INFORMATION:

APPLICANT: NOF CORP.
APPLICANT: NAKAMOTO, Ken-ichiro
APPLICANT: OHASHI, Syunsuke
APPLICANT: YAMAMOTO, Yuji
APPLICANT: SAKANoue, Kenji
APPLICANT: ITOH, Chika
APPLICANT: YASUKOCHI, Tohru
TITLE OF INVENTION: MODIFIED BIO-RELATED SUBSTANCE, PROCESS FOR PRODUCING THE SAME,
FILE REFERENCE: 078575
CURRENT APPLICATION NUMBER: US/10/716,432
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: JP 2003-337113
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
US-10-716-432-1

Query Match 100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPRGSCLLLTSEIDL PVKRR 24
DB 1 MAPRGSCLLLTSEIDL PVKRR 24

RESULT 5
US-10-852-705A-2
Sequence 2, Application US/10852705A
Publication No. US20050191639A1
GENERAL INFORMATION:

APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
TITLE OF INVENTION: Method to isolate genes involved in aging
FILE REFERENCE: RCO/FAC/V098
CURRENT APPLICATION NUMBER: US/10/852,705A
CURRENT FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: EP01204600.9
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION: human HNI CDNA
US-10-852-705A-2

Query Match 100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPRGSCLLLTSEIDL PVKRR 24
DB 1 MAPRGSCLLLTSEIDL PVKRR 24

RESULT 6
US-10-517-956-3
Sequence 3, Application US/10517956
Publication No. US2005023336A1
GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries, Ltd.
TITLE OF INVENTION: Novel Screening Method
FILE REFERENCE: 3067WO0P
CURRENT APPLICATION NUMBER: US/10/517,956
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: JP 2002-173798
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: JP 2002-205470
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 3
LENGTH: 24
TYPE: PRT
ORGANISM: Human
US-10-517-956-3

Query Match 100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPRGSCLLLTSEIDL PVKRR 24
DB 1 MAPRGSCLLLTSEIDL PVKRR 24

RESULT 7
US-10-514-653-1
Sequence 1, Application US/10514653
Publication No. US20050233413A1
GENERAL INFORMATION:
APPLICANT: Nishimoto, Ikuro


```

; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-514-653-1

Query Match      100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MAPRGFSCLLLTSEIDLPVKRR 24
Db 1 MAPRGFSCLLLTSEIDLPVKRR 24

RESULT 8
US-10-514-653-4
; Sequence 4, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: an artificially synthesized polypeptide
; NAME/KEY: MISC FEATURE
; LOCATION: (14)..(14)
; OTHER INFORMATION: The 'Ser' at location 14 stands for phosphorylated Ser.
; US-10-514-653-4

Query Match      100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MAPRGFSCLLLTSEIDLPVKRR 24
Db 1 MAPRGFSCLLLTSEIDLPVKRR 24

RESULT 9
US-10-514-653-5
; Sequence 5, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
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; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: an artificially synthesized polypeptide
; NAME/KEY: MISC FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: The 'Ser' at location 7 stands for phosphorylated Ser.
; US-10-514-653-5

Query Match      100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MAPRGFSCLLLTSEIDLPVKRR 24
Db 1 MAPRGFSCLLLTSEIDLPVKRR 24

RESULT 10
US-10-514-653-6
; Sequence 6, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: an artificially synthesized polypeptide
; NAME/KEY: MISC FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: The 'Ser' at location 7 stands for phosphorylated Ser.
; US-10-514-653-6

Query Match      100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MAPRGFSCLLLTSEIDLPVKRR 24
Db 1 MAPRGFSCLLLTSEIDLPVKRR 24

RESULT 11
US-10-514-653-7
; Sequence 7, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
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; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: an artificially synthesized polypeptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (14)..(14)
; OTHER INFORMATION: The 'Ser' at location 14 stands for D-Ser.
US-10-514-653-7
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Query Match          100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8,1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  MAPRGFSCLLLTSEIDL PVKRR 24
Db      1  MAPRGFSCLLLTSEIDL PVKRR 24
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```

RESULT 12
US-10-514-653-8
; Sequence 8, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: an artificially synthesized polypeptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: The 'Ser' at location 7 stands for D-Ser.
US-10-514-653-8
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Query Match          100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8,1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1  MAPRGFSCLLLTSEIDL PVKRR 24
Db      1  MAPRGFSCLLLTSEIDL PVKRR 24
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RESULT 13
US-10-514-653-9
; Sequence 9, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
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; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: an artificially synthesized polypeptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (7)..(7)
; OTHER INFORMATION: The 'Ser' at location 7 stands for D-Ser.
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (14)..(14)
; OTHER INFORMATION: The 'Ser' at location 14 stands for D-Ser.
US-10-514-653-9
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Query Match          100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8,1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  MAPRGFSCLLLTSEIDL PVKRR 24
Db      1  MAPRGFSCLLLTSEIDL PVKRR 24
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RESULT 14
US-10-514-653-27
; Sequence 27, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 14143-002US1
; CURRENT APPLICATION NUMBER: US/10/514,653
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: PCT/JP03/06139
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/380,958
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-514-653-27
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Query Match          100.0%; Score 120; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 8,1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  MAPRGFSCLLLTSEIDL PVKRR 24
Db      1  MAPRGFSCLLLTSEIDL PVKRR 24
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RESULT 15
US-10-514-653-17
; Sequence 17, Application US/10514653
; Publication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
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;; TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
;; FILE REFERENCE: 14143-002US1
;; CURRENT APPLICATION NUMBER: US/10/514,653
;; CURRENT FILING DATE: 2004-11-15
;; PRIOR APPLICATION NUMBER: PCT/JP03/06139
;; PRIOR FILING DATE: 2003-05-16
;; PRIOR APPLICATION NUMBER: US 60/380,958
;; PRIOR FILING DATE: 2002-05-16
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 17
;; LENGTH: 32
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: an artificially synthesized polypeptide
US-10-514-653-17

Query Match 100.0%; Score 120; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 1,1e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MAPRGFSCLLLTSEIDLPVKRA 24
Db 9 MAPRGFSCLLLTSEIDLPVKRA 32

Search completed: March 28, 2006, 13:26:03
Job time : 14.656 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

COM protein - protein search, using SW model

Run on: March 28, 2006, 13:22:23 ; Search time 1.984 Seconds

(without alignments)
356.787 Million cell updates/sec

Title: US-10-517-956-3

Sequence: 1 MARRGFSCLLTITSEIDLPIVKRRA 24

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Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	24	US-11-142-255-1	Sequence 1, Appl1
2	44	36.7	256	US-11-096-568A-13754	Sequence 13754, A
3	42	35.0	345	US-11-096-568A-356	Sequence 356, App
4	42	35.0	542	US-10-507-755-6	Sequence 6, Appl1
5	40.5	33.8	282	US-10-517-939-346	Sequence 346, App
6	40	33.3	24	US-10-895-064-459	Sequence 459, App
7	40	33.3	24	US-11-129-741-459	Sequence 459, App
8	40	33.3	24	US-11-129-741-3477	Sequence 3477, App
9	40	33.3	79	US-10-746-909-10	Sequence 10, Appl1
10	40	33.3	157	US-10-980-388-73	Sequence 73, Appl1
11	40	33.3	157	US-11-087-099-647	Sequence 647, App
12	40	33.3	178	US-10-511-538-85	Sequence 85, Appl1
13	40	33.3	194	US-11-087-099-3269	Sequence 3269, App
14	39	32.5	44	US-10-467-657-6070	Sequence 6070, App
15	39	32.5	74	US-11-123-896-59	Sequence 59, Appl1
16	39	32.5	74	US-11-123-896-62	Sequence 62, Appl1
17	39	32.5	74	US-11-123-896-65	Sequence 65, Appl1
18	39	32.5	74	US-11-123-896-68	Sequence 68, Appl1
19	39	32.5	84	US-11-096-568A-4498	Sequence 4498, App
20	39	32.5	104	US-11-096-568A-4497	Sequence 4497, App
21	39	32.5	189	US-11-107-029-4	Sequence 4, Appl1
22	39	32.5	311	US-10-980-388-111	Sequence 111, App
23	39	32.5	311	US-10-980-388-113	Sequence 113, App
24	39	32.5	530	US-10-980-388-62	Sequence 62, Appl1
25	39	32.5	689	US-11-087-099-5796	Sequence 5796, App

26	39	32.5	691	7	US-11-087-099-5075	Sequence 5075, App
27	38.5	32.1	92	7	US-11-096-568A-2284	Sequence 2284, App
28	38.5	32.1	95	7	US-11-096-568A-2283	Sequence 2283, App
29	38.5	32.1	154	6	US-10-793-626-602	Sequence 602, App
30	38.5	32.1	316	7	US-11-074-176-358	Sequence 358, App
31	38.5	32.1	332	7	US-11-074-176-230	Sequence 230, App
32	38	31.7	121	6	US-10-644-807-410	Sequence 410, App
33	38	31.7	152	7	US-11-096-568A-677	Sequence 677, App
34	38	31.7	152	7	US-11-096-568A-25508	Sequence 25508, A
35	38	31.7	166	7	US-11-096-568A-676	Sequence 676, App
36	38	31.7	166	7	US-11-096-568A-25507	Sequence 25507, A
37	38	31.7	184	7	US-11-096-568A-12134	Sequence 12134, A
38	38	31.7	191	7	US-11-096-568A-675	Sequence 675, App
39	38	31.7	191	7	US-11-096-568A-25506	Sequence 25506, A
40	38	31.7	248	6	US-10-644-807-326	Sequence 326, App
41	38	31.7	250	6	US-10-131-826A-320	Sequence 320, App
42	38	31.7	250	6	US-10-973-115B-320	Sequence 320, App
43	38	31.7	331	7	US-11-185-878-3	Sequence 3, Appl1
44	38	31.7	335	7	US-11-182-946-7	Sequence 7, Appl1
45	38	31.7	384	7	US-11-087-099-6378	Sequence 6378, App

ALIGNMENTS

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RESULT 1
US-11-142-255-1
Sequence 1, Application US/11142255
Publication No. US20050288490A1
GENERAL INFORMATION:
APPLICANT: NOF CORP.
APPLICANT: NAKAMOTO, Ken-Ichiro
APPLICANT: OHASHI, Syunsuke
APPLICANT: YAMAMOTO, Yuji
APPLICANT: SAKANOUE, Kenji
APPLICANT: ITOH, Chika
APPLICANT: YASUKOCHI, Tohru
TITLE OF INVENTION: MODIFIED BIO-RELATED SUBSTANCE, PROCESS FOR PRODUCING THE SAME,
FILE REFERENCE: 078575
CURRENT APPLICATION NUMBER: US/11/142,255
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/716,432
PRIOR FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: JP 2003-337113
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
US-11-142-255-1
Query Match 100.0%; Score 120; DB 7; Length 24;
Best Local Similarity 100.0%; Pred. No. 1,9e-13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARRGFSCLLTITSEIDLPIVKRRA 24
Db 1 MARRGFSCLLTITSEIDLPIVKRRA 24
RESULT 2
US-11-096-568A-13754
Sequence 13754, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolaï et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
```

;; CURRENT FILING DATE: 2005-04-01
;; NUMBER OF SEQ ID NOS: 34471
;; SEQ ID NO 13754
;; LENGTH: 256
;; TYPE: PRT
;; ORGANISM: Zea mays subsp. mays
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)..(256)
;; OTHER INFORMATION: Cereals Seq. ID no. 12355937
US-11-096-568A-13754

Query Match 36.7%; Score 44; DB 7; Length 256;
Best Local Similarity 36.4%; Pred. No. 8.2;
Matches 12; Conservative 8; Mismatches 3; Indels 10; Gaps 2;

QY 1 MAPRGFSLT-----LITSEIDLPVKRR 24
DB 163 LSPRDW-CLLRPPWQASHLSAQWCLPTRRRA 194

RESULT 3
US-11-096-568A-356
; Sequence 356, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 356
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(345)
; OTHER INFORMATION: Cereals Seq. ID no. 15180242
US-11-096-568A-356

Query Match 35.0%; Score 42; DB 7; Length 345;
Best Local Similarity 64.3%; Pred. No. 24;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 LITSEIDLPVKRR 23
DB 1 LLLPELELPVARR 14

RESULT 4
US-10-507-755-6
; Sequence 6, Application US/10507755
; Publication No. US20060051754A1
; GENERAL INFORMATION:
; APPLICANT: ENDOU, HITOSHI
; APPLICANT: KANAI, YOSHITSUGU
; TITLE OF INVENTION: TRANSPORTER SELECTIVELY TRANSPORTING SULFATE CONJUGATE
; FILE REFERENCE: 61552(71526)
; CURRENT FILING DATE: 2005-09-14
; PRIOR APPLICATION NUMBER: PCT/JP03/02980
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: JP 2002-070985
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 6
; LENGTH: 542
; TYPE: PRT

;; ORGANISM: Homo sapiens
US-10-507-755-6

Query Match 35.0%; Score 42; DB 6; Length 542;
Best Local Similarity 72.7%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 FSCLLLTSRI 16
DB 426 FSCLFLYTSRL 436

RESULT 5
US-10-517-939-346
; Sequence 346, Application US/10517939
; Publication No. US2006003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Betegehlalian, Alireza
; TITLE OF INVENTION: XYLMASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 346
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample.
US-10-517-939-346

Query Match 33.8%; Score 40.5; DB 6; Length 282;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 6 FSCLLLTSRI---DLPV 20
DB 144 FSCLLELVDELLEADVPV 161

RESULT 6
US-10-895-064-459
; Sequence 459, Application US/10895064
; Publication No. US20060018923A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; APPLICANT: LEUNG, FREDERICK C.
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES
; FILE REFERENCE: V0690.0031
; CURRENT FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 2918
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 459
; LENGTH: 24

TYPE: PRT
ORGANISM: Corononavirus-HKU1
US-10-895-064-459

Query Match 33.3%; Score 40; DB 6; Length 24;
Best Local Similarity 64.3%; Pred. No. 3;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 7 SCULLTSEIDLPV 20
||:|||||
Db 1 SCILSTLFISLPV 14

RESULT 7

US-11-129-741-459
Sequence 459, Application US/11129741
Publication No. US20060034853A1
GENERAL INFORMATION:
APPLICANT: YUEN, KWOK YUNG
APPLICANT: WOO, CHIU YAT PATRICK
APPLICANT: LAU, KAR PUI SUSANNA
APPLICANT: CHAN, KWOK HUNG
APPLICANT: POON, LIT MAN
APPLICANT: PEIRIS, JOSEPH S.M.
TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
TITLE OF INVENTION: INFECTION AND USES THEREOF
FILE REFERENCE: V0690.0044
CURRENT FILING DATE: 2005-05-16
PRIOR APPLICATION NUMBER: US/11/129,741
CURRENT FILING DATE: 2005-05-16
PRIOR APPLICATION NUMBER: 10/895,064
NUMBER OF SEQ ID NOS: 4257
SOFTWARE: PatentIn version 3.3
SEQ ID NO 459
LENGTH: 24
TYPE: PRT
ORGANISM: Corononavirus-HKU1
US-11-129-741-459

Query Match 33.3%; Score 40; DB 7; Length 24;
Best Local Similarity 64.3%; Pred. No. 3;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 7 SCULLTSEIDLPV 20
||:|||||
Db 1 SCILSTLFISLPV 14

RESULT 8

US-11-129-741-3477
Sequence 3477, Application US/11129741
Publication No. US20060034853A1
GENERAL INFORMATION:
APPLICANT: YUEN, KWOK YUNG
APPLICANT: WOO, CHIU YAT PATRICK
APPLICANT: LAU, KAR PUI SUSANNA
APPLICANT: CHAN, KWOK HUNG
APPLICANT: POON, LIT MAN
APPLICANT: PEIRIS, JOSEPH S.M.
TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
TITLE OF INVENTION: INFECTION AND USES THEREOF
FILE REFERENCE: V0690.0044
CURRENT FILING DATE: 2005-05-16
PRIOR APPLICATION NUMBER: US/11/129,741
CURRENT FILING DATE: 2005-05-16
PRIOR APPLICATION NUMBER: 10/895,064
NUMBER OF SEQ ID NOS: 4257
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3477
LENGTH: 24
TYPE: PRT

ORGANISM: Corononavirus-HKU1
US-11-129-741-3477

Query Match 33.3%; Score 40; DB 7; Length 24;
Best Local Similarity 64.3%; Pred. No. 3;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 7 SCULLTSEIDLPV 20
||:|||||
Db 1 SCILSTLFISLPV 14

RESULT 9

US-10-746-909-10
Sequence 10, Application US/10746909
Publication No. US2006008873A1
GENERAL INFORMATION:
APPLICANT: Wayne, Robert Thomas
APPLICANT: Chua, Kaw-yan
TITLE OF INVENTION: CLONING AND SEQUENCING OF ALLERGENS OF
TITLE OF INVENTION: DERMATOPHAGOIDES (HOUSE DUST MITE)
FILE REFERENCE: IMI-005CNDV2
CURRENT APPLICATION NUMBER: US/10/746,909
CURRENT FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: 08/175,071
PRIOR FILING DATE: 1993-12-29
PRIOR APPLICATION NUMBER: 08/107,332
PRIOR FILING DATE: 1993-08-16
PRIOR APPLICATION NUMBER: 07/580,655
PRIOR FILING DATE: 1990-09-11
PRIOR APPLICATION NUMBER: 07/458,642
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 79
TYPE: PRT
ORGANISM: Dermatophagoides sp.
US-10-746-909-10

Query Match 33.3%; Score 40; DB 6; Length 79;
Best Local Similarity 69.2%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 SCULLTSEIDLPV 19
||:|||||
Db 9 SCILATSAHDKP 21

RESULT 10

US-10-980-388-73
Sequence 73, Application US/10980388
Publication No. US20050255490A1
GENERAL INFORMATION:
APPLICANT: Vogel, Gabriel
APPLICANT: Parodi, Luis A.
APPLICANT: Hiebsch, Ronald R.
APPLICANT: Lind, Peter
APPLICANT: Kaytes, Paul S.
APPLICANT: Ruff, Valerie
APPLICANT: Ruff, Rita M.
TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl.
FILE REFERENCE: 00325.US1
CURRENT APPLICATION NUMBER: US/10/980,388
CURRENT FILING DATE: 2004-11-02
PRIOR APPLICATION NUMBER: US/09/791,932
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/184,305
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,304
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,303


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; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-73

```

```

Query Match      33.3%; Score 40; DB 6; Length 157;
Best Local Similarity 53.3%; Pred. No. 22;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy      6 FSCLLLTSEIDLPV 20
Db      30 FKCLLPFSEGMV 44

```

```

RESULT 11
US-11-087-099-647
; Sequence 647, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 647
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Trilicium aestivum
US-11-087-099-647

```

```

Query Match      33.3%; Score 40; DB 7; Length 157;
Best Local Similarity 56.2%; Pred. No. 22;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

```

```

Qy      5 GFSCLLLTSEIDLPV 20
Db      41 GFKLELVGLEMV 56

```

```

RESULT 12
US-10-511-538-85
; Sequence 85, Application US/10511538
; Publication No. US20060026700A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: TISSUE SPECIFIC GENES AND GENE CLUSTERS
; FILE REFERENCE: 16U 200 PCT
; CURRENT APPLICATION NUMBER: US/10/511,538
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: US 60/372,669
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,882
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/424,336
; PRIOR FILING DATE: 2002-11-07

```

```

; PRIOR APPLICATION NUMBER: US 60/374,823
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/376,558
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 60/381,366
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/403,648
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-538-85

```

```

Query Match      33.3%; Score 40; DB 6; Length 178;
Best Local Similarity 56.2%; Pred. No. 25;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      9 LLILTSEIDLPVKRA 24
Db      91 VILITSELPVPYRS 106

```

```

RESULT 13
US-11-087-099-3269
; Sequence 3269, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3269
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Trilicium aestivum
US-11-087-099-3269

```

```

Query Match      33.3%; Score 40; DB 7; Length 194;
Best Local Similarity 56.2%; Pred. No. 28;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

```

```

Qy      5 GFSCLLLTSEIDLPV 20
Db      81 GFKLELVGLEMV 96

```

```

RESULT 14
US-10-467-657-6070
; Sequence 6070, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6070
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae

```

US-10-467-657-6070

Query Match 32.5%; Score 39; DB 6; Length 44;
 Best Local Similarity 50.0%; Pred. No. 8.3;
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 6 FSCLLLTSEIDLPVKR 23
 ||||| : ||
 Db 7 FSCILLLELLIKVLLKNR 24

RESULT 15

US-11-123-896-59
 ; Sequence 59, Application US/11123896
 ; Publication No. US20050273881A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Simmons, Carl R.
 ; APPLICANT: Navarro Acevedo, Pedro A.
 ; APPLICANT: Harvell, Leslie
 ; APPLICANT: Cahoon, Rebecca
 ; APPLICANT: McCutchen, Billy Fred
 ; APPLICANT: Lu, Albert
 ; APPLICANT: Herrmann, Rafael
 ; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
 ; TITLE OF INVENTION: Use
 ; FILE REFERENCE: 35718/246703
 ; CURRENT APPLICATION NUMBER: US/11/123,896
 ; CURRENT FILING DATE: 2005-05-06
 ; PRIOR APPLICATION NUMBER: 60/300,152
 ; PRIOR FILING DATE: 2001-06-22
 ; PRIOR APPLICATION NUMBER: 60/300,241
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 469
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 59
 ; LENGTH: 74
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 US-11-123-896-59

Query Match 32.5%; Score 39; DB 7; Length 74;
 Best Local Similarity 55.6%; Pred. No. 15;
 Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 5 GFSCLLTSEIDLPVKR 22
 ||||| : |||
 Db 7 GFLFLLLVLTASDVTVKR 24

Search completed: March 28, 2006, 13:26:39
 Job time : 1.984 secs

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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:10:18 ; Search time 252.72 Seconds
(without alignments)
610.248 Million cell updates/sec

Title: US-10-517-956-1
Perfect score: 1817
Sequence: 1 METNFSPTPLNXYEVSYESA.....TNDTAANSASPAAETELQAM 351

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1817	100.0	351	5	AAU79035 Human for
2	1817	100.0	351	6	ABU89747 Protein d
3	1817	100.0	351	6	ABP81818 Human for
4	1817	100.0	351	7	ADG89689 Human for
5	1817	100.0	351	8	ADH58975 Human GPC
6	1817	100.0	351	8	ADH53315 Human GPC
7	1817	100.0	351	8	ADO29691 Human GPC
8	1817	100.0	351	8	ADP12531 Protein e
9	1817	100.0	351	8	ADG57846 Human for
10	1817	100.0	351	8	ADP24410 PRO polyp
11	1817	100.0	351	8	ADG74158 Human LXA
12	1817	100.0	351	9	ADG06859 CycLin-de
13	1817	100.0	351	9	ADY73233 Human FPR
14	1817	100.0	351	9	AEA27939 Human for
15	1817	100.0	370	6	ABU10071 Human G-P
16	1815	99.9	702	9	ADY73573 Human FPR
17	1815	99.7	351	4	ABBS6354 Non-endog
18	1744	96.0	351	9	ADY73577 Human FPR
19	1725	94.9	351	9	ADY73576 Human FPR
20	1688	92.9	326	6	ABU10072 Human HGP
21	1594	87.7	325	8	ABU10073 Human HGP
22	1420	78.2	351	8	ADH58986 Mouse GPC
23	1420	78.2	351	8	ADH53333 Mouse FPR
24	1420	78.2	351	8	ADO29714 Mouse GPC

25	1420	78.2	351	8	ADO57850 Mouse for
26	1419	78.1	351	8	ADH58984 Rat GPCR
27	1419	78.1	351	8	ADH53331 Rat FPR1
28	1419	78.1	351	8	ADO57848 Rat formy
29	1327	73.0	353	5	ABG95152 Human GPC
30	1327	73.0	353	8	ADG64561 Human FPR
31	1327	73.0	413	8	ADG64565 Human N-E
32	1327	72.9	591	7	ADP70495 Orphan re
33	1325	72.9	347	8	ADO29713 Mouse GPC
34	1321	72.7	353	5	ABG95161 Human GPC
35	1321	72.7	353	8	ADG64571 Human FPR
36	1318	72.5	353	6	ABP81729 Human for
37	1318	72.5	353	7	ADD32067 Human for
38	1318	72.5	353	8	ADH58988 Human GPC
39	1318	72.5	353	8	ADH53335 Human FPR
40	1318	72.5	353	8	ADO29692 Human GPC
41	1318	72.5	353	8	ADP24713 PRO polyp
42	1318	72.5	353	8	ADH57056 Human 155
43	1318	72.5	353	8	ADU01527 Human G P
44	1318	72.5	353	9	ADY73235 Human FPR
45	1316	72.4	353	9	ADY73575 Human FPR

ALIGNMENTS

RESULT 1	AAU79035	AAU79035 standard; protein; 351 AA.
ID	AAU79035	
AC	AAU79035;	
DT	18-JUN-2002 (first entry)	
XX		
DE	Human formyl peptide receptor like-1 receptor, FPR1-1.	
XX		
KW	Human; FPR1-1; formyl peptide receptor like-1; receptor; ILM receptor;	
KW	macrophage surface receptor; antiinflammatory; pulmonary;	
KW	chronic inflammatory airway disease; chronic bronchitis;	
KW	chronic obstructive pulmonary disease; COPD.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200218938-A1.	
XX		
PD	07-MAR-2002.	
XX		
PF	23-AUG-2001; 2001WO-EP009727.	
XX		
PR	01-SEP-2000; 2000GB-00021484.	
XX		
PA	(BOEH) BOEHRINGER INGELHEIM PHARMA KG.	
XX		
PI	Jung B, Kraut N, Mueller S, Kistler B, Seither P, Quast K;	
XX	Weith A;	
XX	WPI; 2002-315580/35.	
DR	N-PDB; ABK48101.	
XX		
PT	Determining an expression level of ILM (a macrophage surface receptor),	
PT	for the diagnosis or monitoring of chronic inflammatory airway disease,	
PT	comprises determining the level of the ILM receptor expressed in a	
PT	macrophage.	
XX		
PS	Claim 7; Page 49-51; 79pp; English.	
XX		
CC	The invention relates to determining an expression level of an ILM	
CC	receptor (macrophage surface receptor), comprises determining the level	
CC	of an ILM receptor expressed in a macrophage. Also included are a method	
CC	of determining whether a substance is an activator or an inhibitor of an	
CC	ILM receptor, involving applying the substance to a test system which	
CC	generates a measurable read-out upon modulation of the ILM receptor or an	
CC	ILM receptor function, a test system for determining whether a substance	

CC is an activator or an inhibitor of an ILM receptor function,
 CC characterised in that the receptor is involved in a chronic inflammatory
 CC atway disease and where the receptor plays a role in mediating
 CC inflammation comprising: (i) an ILM receptor; (ii) an expression vector
 CC capable of expressing an ILM receptor in a cell; or (iii) a host cell
 CC transformed with an expression vector capable of expressing the ILM
 CC receptor and a substance determined to be an activator or inhibitor of an
 CC ILM receptor. The methods are useful for the diagnosis or monitoring of a
 CC chronic inflammatory airway disease, e.g. chronic bronchitis and chronic
 CC obstructive pulmonary disease (COPD). The substance determined to be an
 CC activator or inhibitor of an ILM receptor, is useful for treating the
 CC diseases and for modulating an ILM receptor in a macrophage. The present
 CC sequence is an ILM receptor which is differentially expressed and which
 CC is involved in causing the induction and/or maintenance of the
 CC hyperactive status of macrophages involved in an inflammatory process

XX Sequence 351 AA:

Query Match 100.0%; Score 1817; DB 5; Length 351;
 Best Local Similarity 100.0%; Pred. No. 7.8e-196;
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFSPTLNEYBEVSEYASGYTVLRILPLVVLGTVFVLGVNGLVIVWAGFRMRTTYT 60
 DB 1 METNFSPTLNEYBEVSEYASGYTVLRILPLVVLGTVFVLGVNGLVIVWAGFRMRTTYT 60
 QY 61 TICVNLALADFSFTATLPFLIVSMAMGEKMPGFLCKLHIIVDINLFGSVPLIGFIA 120
 DB 61 TICVNLALADFSFTATLPFLIVSMAMGEKMPGFLCKLHIIVDINLFGSVPLIGFIA 120
 QY 121 LDRICICVLAHVAQNHRITVSLAMKVIYGPWIALVLTLPVFLFTVTIPNGDTYCTENF 180
 DB 121 LDRICICVLAHVAQNHRITVSLAMKVIYGPWIALVLTLPVFLFTVTIPNGDTYCTENF 180
 QY 181 ASNGGTPBERLKVATITMLTARGIIRFVIGFSIPMSIVAICYGLIAAKIHKKMIKSRPL 240
 DB 181 ASNGGTPBERLKVATITMLTARGIIRFVIGFSIPMSIVAICYGLIAAKIHKKMIKSRPL 240
 QY 241 RVLTAIVASFFICMPFPQVALIGTWLKEMLFYGKKYKIDILVNPTSSLAFFNSCLNPM 300
 DB 241 RVLTAIVASFFICMPFPQVALIGTWLKEMLFYGKKYKIDILVNPTSSLAFFNSCLNPM 300
 QY 301 LYPVVGODFRERLIHSLPTSLERALSBDSPNTDPAANSASPPAETELQAM 351
 DB 301 LYPVVGODFRERLIHSLPTSLERALSBDSPNTDPAANSASPPAETELQAM 351

RESULT 2

ABU89747
 ID ABU89747 standard; protein; 351 AA.

XX AC ABU89747;

XX DT 10-JUL-2003 (first entry)

XX DE Protein differentially expressed in cardiovascular disease #41.

XX KM Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;
 KM myocardial infarction; candida; antiarteriosclerotic; antianginal;
 KM gene therapy; differential gene expression.

XX OS Homo sapiens.

XX PN MO2003031650-A2.

XX PD 17-APR-2003.

XX PF 02-OCT-2002; 2002MO-EP011034.

XX PR 08-OCT-2001; 2001GB-00024145.

XX PA (PAB) BAYER AG.

XX XX

PI Munsee M, Gehrmann M, Wick M, Schmitz G;

XX WPI; 2003-403108/38.

DR N-PSDB; ACA89920.

XX

PT Predicting, diagnosing or prognosing a cardiovascular disease, e.g.

PT angina, ischaemia, myocardial infarction or arteriosclerosis by detection

PT of a polynucleotide in a biological sample comprising detecting a

PT hybridization complex.

XX

PS Claim 3; Page 375-377; 454pp: English.

CC The invention describes a method of predicting, diagnosing or prognosing

CC a cardiovascular disease by detection of a polynucleotide in a biological

CC sample comprising hybridizing at least one of the polynucleotide to a

CC nucleic acid material of a biological sample, thus forming a

CC hybridization complex, and detecting the hybridization complex. The

CC polynucleotides, polypeptides, antisense molecule, antibody and reagent

CC are useful for preparing compositions for preventing, predicting or

CC diagnosing, or a medicament for treating a cardiovascular disease, e.g.

CC arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction.

CC This sequence represents a protein identified in the invention as being

CC differentially expressed in individuals with cardiovascular disease

XX Sequence 351 AA;

Query Match 100.0%; Score 1817; DB 6; Length 351;
 Best Local Similarity 100.0%; Pred. No. 7.8e-196;
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFSPTLNEYBEVSEYASGYTVLRILPLVVLGTVFVLGVNGLVIVWAGFRMRTTYT 60
 DB 1 METNFSPTLNEYBEVSEYASGYTVLRILPLVVLGTVFVLGVNGLVIVWAGFRMRTTYT 60
 QY 61 TICVNLALADFSFTATLPFLIVSMAMGEKMPGFLCKLHIIVDINLFGSVPLIGFIA 120
 DB 61 TICVNLALADFSFTATLPFLIVSMAMGEKMPGFLCKLHIIVDINLFGSVPLIGFIA 120
 QY 121 LDRICICVLAHVAQNHRITVSLAMKVIYGPWIALVLTLPVFLFTVTIPNGDTYCTENF 180
 DB 121 LDRICICVLAHVAQNHRITVSLAMKVIYGPWIALVLTLPVFLFTVTIPNGDTYCTENF 180
 QY 181 ASNGGTPBERLKVATITMLTARGIIRFVIGFSIPMSIVAICYGLIAAKIHKKMIKSRPL 240
 DB 181 ASNGGTPBERLKVATITMLTARGIIRFVIGFSIPMSIVAICYGLIAAKIHKKMIKSRPL 240
 QY 241 RVLTAIVASFFICMPFPQVALIGTWLKEMLFYGKKYKIDILVNPTSSLAFFNSCLNPM 300
 DB 241 RVLTAIVASFFICMPFPQVALIGTWLKEMLFYGKKYKIDILVNPTSSLAFFNSCLNPM 300
 QY 301 LYPVVGODFRERLIHSLPTSLERALSBDSPNTDPAANSASPPAETELQAM 351
 DB 301 LYPVVGODFRERLIHSLPTSLERALSBDSPNTDPAANSASPPAETELQAM 351

RESULT 3

ABP81818
 ID ABP81818 standard; protein; 351 AA.

XX AC ABP81818;

XX DT 04-MAR-2003 (first entry)

XX DE Human formyl peptide receptor-like receptor protein SEQ ID NO:120.

XX KM G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

XX G protein-coupled receptor; modulator; antibody; immune-related disease;

XX growth-related disease; cell regeneration-related disease; AIDS; cancer;

XX immunological-related disease; cell proliferative disease; autoimmune disease;

XX Alzheimer's disease; arteriosclerosis; infection; osteoarthritis; allergy;

XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;

XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

KM mental retardation; epilepsy; aschma; tuberculosis; obesity; nausea;
 KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 XX ulcer.
 OS Homo sapiens.
 XX
 XX WO200261087-A2.
 PN
 XX
 XX 08-AUG-2002.
 P2
 XX
 PF 19-DEC-2001; 2001WO-US050107.
 *XX
 PR 19-DEC-2000; 2000US-0257144P.
 XX
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 PA
 XX
 PI Burner GC, Roush CL, Brown JP;
 XX
 DR WPI; 2003-046718/04.
 DR N-PSDB; ABZ4264.
 XX
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX
 XX Disclosure; Fig 1; 523pp; English.

CC The present invention describes antigenic peptide (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABP82523 to ABP82869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention

Query Match	100.0%	Score 1817	DB 6	Length 351
Best Local Similarity	100.0%	Pred. NO. 7.8e-196		
Matches 351	0	Mismatches 0	Indels 0	Gaps 0
Conservative				

QY 1 METNFSTPLNLEYEEVSYESAGYVTLRLPLVLGATFVLGLANGLYIWAGFRMTRVT 60

Db 1 METNFSTPLNLEYEEVSYESAGYVTLRLPLVLGATFVLGLANGLYIWAGFRMTRVT 60

QY 61 TICLNALADFSFATLPLPLIYSMAMGEEKPMGPICTKIHHVVDINLFGSFFLGFIA 120

Db 61 TICLNALADFSFATLPLPLIYSMAMGEEKPMGPMCTKIHHVVDINLFGSFFLGFIA 120

QY 121 LDRICCYLHPVMAQNHRVTSLAMKVIGPMILAVTLPLPELFTTYTINPGDYTCFEN 180

Db 121 LDRICCYLHPVMAQNHRVTSLAMKVIGPMILAVTLPLPELFTTYTINPGDYTCFEN 180

QY 181 ASMGCTEERBUKVAITLTLTGRIIRFVIGSLPSMISVAICYGLIAAKIHKKGKIKSSRPL 240

D6	181	ASMGCTPEERLKAITMLTARGIIRFVIGFSIPMSIVAI CYGLNAAKHKKGMKSSRPL	240
OY	241	RVTAVAVASEFFICMPFOVLALGTVMLEKMFYKYKI IDILVNPTSLAFNSCINPM	300
Db	241	RVLTAVASFFICMFPFOVLALGTVMLEKMFYKYKI IDILVNPTSLAFNSCINPM	300
OY	301	LYYFGODPFRRLIHSLPTSLERALSEDSAPNTDPAANSASPAPTELOAM	351
Db	301	LYYFGODPFRRLIHSLPTSLERALSEBSAPNTDPAANSASPAPTELOAM	351

```

RESULT 4
ADC89689
ID ADC89689 standard; protein; 351 AA.
XX
AC ADC89689;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human formyl peptide receptor-like 1 (FPR1), SEQ ID NO.2.

```

Human, formyl peptide receptor-like 1, FPR1; G protein coupled receptor GPCR; drug screening; diagnosis; haematological disease; cardiovascular disease; peripheral nervous system disease; central nervous system disease; respiratory disease; chronic obstructive pulmonary disease, COPD, asthma; geriatric-urological disease; inflammatory disease; neuroprotective; cardiac; respiratory; antiasthmatic; antiinflammatory; gene therapy; receptor.

OS Homo sapiens.
 XX
 PN WO2003083314-A2.
 XX
 XX
 PD 09-OCT-2003.
 XX
 XX
 PF 21-MAR-2003; 2003WO-EP002959
 XX
 XX
 PR 03-APR-2002; 2002EP-00007291

AA	(FARB) BAYER AG.	
PA		
XX		
PI	Golz S, Brueggemeier U, Geerts A,	
XX		
DR	WPI, 2003-803965/75.	
DR	N-PSDB; ADC89688.	

PT Screening for therapeutic agents for treating a disease e.g.,
PT cardiovascular, inflammatory, or respiratory diseases by contacting a
PT test compound with a FPR1 polypeptide or polynucleotide and detecting
PT binding of the test compound.

PS Disclosure; SEQ ID NO 2; 119pp; English.

The invention relates to a method of screening for agents for treating foetal peptide receptor-like 1 (FPR1)-related disorders in a mammal. The method involves detecting the binding of test compound to an FPR1 polypeptide or polynucleotide, or determining the activity of an FPR1 polypeptide at different concentrations of the test compound. FPR1 is a G protein coupled receptor (GPCR) which is highly expressed in a variety of human tissues. It is expressed in various brain tissues, cardiovascular system tissues, erythrocytes and other haematological tissues, respiratory tissues, genito-urological tissues such as prostate and placenta, and in various immune system tissues. In particular, it is expressed at a higher level in lungs affected with chronic obstructive pulmonary disease (COPD), compared with healthy lungs. The invention also encompasses a method of diagnosing an FPR1-related disorder by quantification of FPR1 polynucleotides, and pharmaceutical compositions for treating an FPR1-related disorder. Therapeutic agents identified using the method of the invention can be used in the treatment of disorders such as haematological diseases, cardiovascular diseases, peripheral and central nervous system diseases, respiratory diseases

CC (e.g., COPD), asthma, genito-urological diseases, or inflammatory
 CC diseases. The present sequence represents human FPR1 protein.

XX Sequence 351 AA:

Query Match 100.0%; Score 1817; DB 7; Length 351;
 Best Local Similarity 100.0%; Pred. No. 7,8e-196;
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEYEEVESAGYTVLRILPLVVGTVFVLGNGLVIMVAGFRMTRTVT 60
 DB 1 METNFTPLNEYEEVESAGYTVLRILPLVVGTVFVLGNGLVIMVAGFRMTRTVT 60
 QY 61 TTCYLNALADSFYATLPFLIVSMAMGKMPGWFCLKIHIIVDINLFGSVFLIGFLA 120
 DB 61 TTCYLNALADSFYATLPFLIVSMAMGKMPGWFCLKIHIIVDINLFGSVFLIGFLA 120
 QY 121 LDRICVLRPWAQNRRVTSIAKVIYGPWILALVLTLPFLFTVTTPNGDTYCTENF 180
 DB 121 LDRICVLRPWAQNRRVTSIAKVIYGPWILALVLTLPFLFTVTTPNGDTYCTENF 180
 QY 181 ASWGGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKMIKSSRPL 240
 DB 181 ASWGGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKMIKSSRPL 240
 QY 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYGYKKIIDILVNPTSSIAFPNSCLNPM 300
 DB 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYGYKKIIDILVNPTSSIAFPNSCLNPM 300
 QY 301 LVYFVGQDPRERLIHSLPTSLERALSDESAPTNDTAAASAPPAETELQAM 351
 DB 301 LVYFVGQDPRERLIHSLPTSLERALSDESAPTNDTAAASAPPAETELQAM 351

RESULT 5

ID ADH58975 standard; protein; 351 AA.

XX ADH58975;

XX 25-MAR-2004 (first entry)

DE Human GPCR related amino acid sequence #SEQ ID 1.

XX Neotropic; antiparkinsonian; neuroprotective; antidiabetic;
 KM G-protein coupled humanin receptor; agonist; antagonist; humanin;
 KM G-protein coupled receptor protein; GPCR; FPR1; FPR2; nerve; brain;
 KM Alzheimer's disease; Parkinson's disease; Huntington's disease;
 KM Down's syndrome; prion disease; muscular dystrophy; multiple sclerosis;
 KM Creutzfeldt-Jacob disease; neuroblastoma.

XX Homo sapiens.

XX WO2003106683-A1.

XX 24-DEC-2003.

XX 12-JUN-2003; 2003WO-JP007500.

XX 14-JUN-2002; 2002JP-00173798.

XX 15-JUL-2002; 2002JP-00205470.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Hinuma S, Fujii R, Harada M, Hosoya M;

XX WPI, 2004-108321/11.

PT Screening potential humanin receptor agonists and antagonists using
 PT humanin and G-coupled receptor protein FPR1 or FPR2 for apoptosis
 PT regulation and treatment and prevention of disorders of nerve and brain
 PT function.

PS Claim 1; SEQ ID NO 1; 160pp; Japanese.

XX The invention relates to a method for screening compounds and their salts
 CC which modify the binding properties and signal transduction of humanin
 CC and its salts with humanin receptor protein and its salts, using humanin
 CC or its salts together with G-protein coupled receptor protein FPR1 or
 CC FPR2 or its partial peptides or salts or proteins of equivalent
 CC activity. The method of the invention is useful in the treatment and
 CC prevention of disorders of nerve and brain function, including
 CC Alzheimer's disease, Parkinson's disease, Huntington's disease, Down's
 CC syndrome, prion diseases, muscular dystrophy, diabetic neuropathy,
 CC multiple sclerosis, cerebral sclerosis, cerebral hemorrhage, cerebral
 CC ischemia, subdural hematoma, Creutzfeldt-Jacob disease, neuroblastoma,
 CC neuropathy associated with viral (including HIV), protozoal or Rickettsia
 CC infections, and neuropathy associated with vaccination. The current
 CC sequence represents a human G-protein coupled receptor protein related
 CC amino acid sequence.

XX Sequence 351 AA:

Query Match 100.0%; Score 1817; DB 8; Length 351;
 Best Local Similarity 100.0%; Pred. No. 7,8e-196;
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEYEEVESAGYTVLRILPLVVGTVFVLGNGLVIMVAGFRMTRTVT 60
 DB 1 METNFTPLNEYEEVESAGYTVLRILPLVVGTVFVLGNGLVIMVAGFRMTRTVT 60
 QY 61 TTCYLNALADSFYATLPFLIVSMAMGKMPGWFCLKIHIIVDINLFGSVFLIGFLA 120
 DB 61 TTCYLNALADSFYATLPFLIVSMAMGKMPGWFCLKIHIIVDINLFGSVFLIGFLA 120
 QY 121 LDRICVLRPWAQNRRVTSIAKVIYGPWILALVLTLPFLFTVTTPNGDTYCTENF 180
 DB 121 LDRICVLRPWAQNRRVTSIAKVIYGPWILALVLTLPFLFTVTTPNGDTYCTENF 180
 QY 181 ASWGGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKMIKSSRPL 240
 DB 181 ASWGGTPEERLKVATITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKMIKSSRPL 240
 QY 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYGYKKIIDILVNPTSSIAFPNSCLNPM 300
 DB 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYGYKKIIDILVNPTSSIAFPNSCLNPM 300
 QY 301 LVYFVGQDPRERLIHSLPTSLERALSDESAPTNDTAAASAPPAETELQAM 351
 DB 301 LVYFVGQDPRERLIHSLPTSLERALSDESAPTNDTAAASAPPAETELQAM 351

RESULT 6

ID ADI53315 standard; protein; 351 AA.

XX ADI53315;

XX 22-APR-2004 (first entry)

DE Human FPR1 transmembrane G-protein coupled receptor.

XX screening; binding; signal transduction;
 KM humanin-like peptide receptor protein; G-protein coupled receptor; FPR1;
 KM FPR2; transmembrane G-protein coupled receptor; nervous system disorder;
 KM Alzheimer's disease; Parkinson's disease; Down's syndrome;
 KM Huntington's disease; muscular dystrophy; prion disease;
 KM Creutzfeldt-Jacob disease; diabetic neuropathy; multiple sclerosis;
 KM cerebral ischemia; apoplexy; brain haemorrhage;
 KM subarachnoid haemorrhage; human.

XX Homo sapiens.

XX WO2004008141-A1.

XX 22-JAN-2004.

XX 12-JUN-2003; 2003MO-JP007501.
XX PF
XX 15-JUL-2002; 2002JP-00205554.
XX PR
XX (TAKEDA) TAKEDA CHEM IND LTD.
XX PA
XX Hihnuma S, Fujii R, Harada M, Hosoya M, Mori M,
XX WPI; 2004-143116/14.
XX DR N-PSDB; ADI53316.
XX
PT Screening compounds modifying binding of humanin-like peptide to its
PT receptor protein for identification of apoptosis regulators and remedies
PT for nervous system disorders, e.g. Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 1; 116pp; Japanese.
XX
CC The invention comprises a method for screening for compounds which modify
CC the binding or signal transmission of humanin-like peptide receptor
CC protein (a G-protein coupled receptor). The method involves the use of
CC human, rat or mouse FPR1/FPR2 transmembrane G-protein coupled receptor.
CC The compounds isolated by the method of the invention are useful for the
CC treatment and prevention of nervous system disorders (e.g. Alzheimer's
CC disease, Parkinson's disease, Down's syndrome, Huntington's disease,
CC muscular dystrophy, prion disease, Creutzfeldt-Jacob disease, diabetic
CC neuropathy, multiple sclerosis, cerebral ischaemia, apoplexy, brain
CC haemorrhage and subarachnoid haemorrhage). The present amino acid
CC sequence represents a human FPR1 protein.
XX
SQ Sequence 351 AA;
XX
Query Match 100.0%; Score 1817; DB 8; Length 351;
Best Local Similarity 100.0%; Pred. No. 7, 8e-196;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MERNFSTPLNBYEBSYESAGYVLRLLPLVLTGTVLGVNGLYVWAGFRMTTWT 60
DB 1 METNFSPLNBYEBSYESAGYVLRLLPLVLTGTVLGVNGLYVWAGFRMTTWT 60
XX
QY TITCYLNLALDPSFATPLPLIYVSMANGKMPGMPFLCKLHIVDNLNGSVPLGFIA 120
DB 61 TITCYLNLALDPSFATPLPLIYVSMANGKMPGMPFLCKLHIVDNLNGSVPLGFIA 120
XX
QY 121 LDRICVLAHPVMAQNHTVSLAMKVIVGPIALVLTLPVFLFTVTIENGDTYCTFNF 180
DB 121 LDRICVLAHPVMAQNHTVSLAMKVIVGPIALVLTLPVFLFTVTIENGDTYCTFNF 180
XX
QY 121 LDRICVLAHPVMAQNHTVSLAMKVIVGPIALVLTLPVFLFTVTIENGDTYCTFNF 180
DB 121 LDRICVLAHPVMAQNHTVSLAMKVIVGPIALVLTLPVFLFTVTIENGDTYCTFNF 180
XX
QY 181 ASWNGTPEERBLKVAITMLTARGIIRFYIGSLPMSIYVLCYGLIAKIHKKGMKSSRPL 240
DB 181 ASWNGTPEERBLKVAITMLTARGIIRFYIGSLPMSIYVLCYGLIAKIHKKGMKSSRPL 240
XX
QY 181 ASWNGTPEERBLKVAITMLTARGIIRFYIGSLPMSIYVLCYGLIAKIHKKGMKSSRPL 240
DB 181 ASWNGTPEERBLKVAITMLTARGIIRFYIGSLPMSIYVLCYGLIAKIHKKGMKSSRPL 240
XX
QY 241 RVLTAIVASFFICMPFPQVALLGTVLWKLMPGKKIIDIIVNPFSSLAFFNSCLNPM 300
DB 241 RVLTAIVASFFICMPFPQVALLGTVLWKLMPGKKIIDIIVNPFSSLAFFNSCLNPM 300
XX
QY 241 RVLTAIVASFFICMPFPQVALLGTVLWKLMPGKKIIDIIVNPFSSLAFFNSCLNPM 300
DB 241 RVLTAIVASFFICMPFPQVALLGTVLWKLMPGKKIIDIIVNPFSSLAFFNSCLNPM 300
XX
QY 301 LYVFGVGDPEERBLIHSPLTSLERLSDSAPTVNDTANASAPPAETELQAM 351
DB 301 LYVFGVGDPEERBLIHSPLTSLERLSDSAPTVNDTANASAPPAETELQAM 351
XX
RESULT 7
ADO29691
ID ADO29691 standard; protein; 351 AA.
XX
XX ADO29691;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human GPCR FPR1, SEQ ID NO:193.
XX
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
XX transgenic mouse; neurological disorder; adrenal gland disorder;
XX

KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antineurotic;
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW receptor.
XX
XX Homo sapiens.
XX
XX WO2004040000-A2.
XX
PD 13-MAY-2004.
XX
XX
XX 09-SEP-2003; 2003MO-US028226.
XX PF
XX 09-SEP-2002; 2002US-0409303P.
XX PR
XX 09-APR-2003; 2003US-0461329P.
XX
XX (PRIM-) PRIMAL INC.
XX
XX Galtenaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F,
PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
PI WPI; 2004-390329/36.
XX
XX N-PSDB; ADO30066.
XX
DR Novel mammalian G protein coupled receptors, useful for identifying
XX compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX
PS Claim 15; SEQ ID NO 793; 542pp; English.
XX
XX The invention relates to human and mouse G protein-coupled receptors
XX (GPCRs) and nucleic acids encoding them. The invention also relates to
XX sequences at least 90% identical to the GPCR proteins and nucleic acids
XX of the invention; methods of treating, preventing or diagnosing diseases
XX associated with GPCRs of the invention; methods of screening for
XX compounds useful in the treatment of GPCR-related diseases; a transgenic
XX mouse comprising a GPCR gene of the invention; a mouse comprising a
XX mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
XX from the transgenic mice; kits comprising several mice, each of which has
XX a mutation in a different GPCR gene of the invention; and kits comprising
XX probes which hybridise to GPCR polynucleotides of the invention. The
XX invention further discloses variants of the GPCR polypeptides and vectors
XX comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
XX be used in the diagnosis, treatment or prevention of a wide variety of
XX diseases including neurological disorders (e.g., Alzheimer's disease,
XX depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
XX disorders of the adrenal gland; disorders of the colon or intestine
XX (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
XX syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
XX myocardial infarction); muscular disorders (e.g., autoimmune disorders or
XX anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
XX AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
XX arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
XX obesity, enzyme deficiency-related diseases or vitamin deficiency-related
XX diseases); and disorders of the kidney, liver, lung, breast, ovary,
XX uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
XX thyroid (e.g., cancers). The present sequence represents a GPCR of the
XX invention. Note: The full sequence data for this patent did not form part
XX of the printed specification; those sequences not shown were obtained in
XX ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 351 AA;
XX

Query Match 100.0%; Score 1817; DB 8; Length 351;
 Best Local Similarity 100.0%; Pred. No. 7.8e-196;
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 METNSTPLNEVEEVSYESAGYTVLRILPLVVLGVTFLVGLGNGLVIVWAGFRMTRTVT 60
 1 METNSTPLNEVEEVSYESAGYTVLRILPLVVLGVTFLVGLGNGLVIVWAGFRMTRTVT 60
 Db 1 METNSTPLNEVEEVSYESAGYTVLRILPLVVLGVTFLVGLGNGLVIVWAGFRMTRTVT 60

QY 61 TTCYLNALADPSFTATLPPLIVSMAMGKMPFGWFLCKLHIIVVDINLFGSVFLIGFIA 120
 Db 61 TTCYLNALADPSFTATLPPLIVSMAMGKMPFGWFLCKLHIIVVDINLFGSVFLIGFIA 120

QY 121 LDRCTCVLHPVMAQNRHTVSLAMKVIVGPMIALVLTLPVPLFTVTTPNGDTCTENF 180
 Db 121 LDRCTCVLHPVMAQNRHTVSLAMKVIVGPMIALVLTLPVPLFTVTTPNGDTCTENF 180

QY 181 ASWGTPPEERLKVATMTLARGIIRFVIGFSLPMSIVAICYGLIAKIHKKMIKSSRPL 240
 Db 181 ASWGTPPEERLKVATMTLARGIIRFVIGFSLPMSIVAICYGLIAKIHKKMIKSSRPL 240

QY 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYGYKKIIDILVNPTSLAFNSCLNPM 300
 Db 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYGYKKIIDILVNPTSLAFNSCLNPM 300

QY 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDPAANSASPPAETELQAM 351
 Db 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDPAANSASPPAETELQAM 351

RESULT 8
 ADP12531
 ID ADP12531 standard; protein; 351 AA.
 AC ADP12531;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Protein encoded by mRNA of the invention #141.
 XX
 KW transplamt rejection; immune system; rheumatoid arthritis; lupus;
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
 XX
 OS Homo sapiens.
 OS
 PN WO2004042346-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 24-APR-2003; 2003WO-US012946.
 XX
 PR 24-APR-2002; 2002US-00131831.
 PR 20-DEC-2002; 2002US-00325899.
 XX
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX
 PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 PI Rosenberg S;
 XX
 DR WPI; 2004-400724/37.
 XX
 PA Diagnosing or monitoring transplamt rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplamt
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.
 XX
 PS Claim 65; SEQ ID NO 2540; 1762bp; English.
 XX
 CC The present invention relates to diagnosing or monitoring transplamt
 CC rejection, e.g. cardiac or kidney transplamt rejection, in an individual
 CC comprises detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplamt rejection, e.g. heart, kidney, liver, pancreas, pancreatic

CC islet, lung, bone marrow or stem cell transplamt rejection,
 CC xenotransplamt rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC protein that is encoded by the mRNA of the invention.
 CC
 SQ Sequence 351 AA;

Query Match 100.0%; Score 1817; DB 8; Length 351;
 Best Local Similarity 100.0%; Pred. No. 7.8e-196;
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 METNSTPLNEVEEVSYESAGYTVLRILPLVVLGVTFLVGLGNGLVIVWAGFRMTRTVT 60
 1 METNSTPLNEVEEVSYESAGYTVLRILPLVVLGVTFLVGLGNGLVIVWAGFRMTRTVT 60
 Db 1 METNSTPLNEVEEVSYESAGYTVLRILPLVVLGVTFLVGLGNGLVIVWAGFRMTRTVT 60

QY 61 TTCYLNALADPSFTATLPPLIVSMAMGKMPFGWFLCKLHIIVVDINLFGSVFLIGFIA 120
 Db 61 TTCYLNALADPSFTATLPPLIVSMAMGKMPFGWFLCKLHIIVVDINLFGSVFLIGFIA 120

QY 121 LDRCTCVLHPVMAQNRHTVSLAMKVIVGPMIALVLTLPVPLFTVTTPNGDTCTENF 180
 Db 121 LDRCTCVLHPVMAQNRHTVSLAMKVIVGPMIALVLTLPVPLFTVTTPNGDTCTENF 180

QY 181 ASWGTPPEERLKVATMTLARGIIRFVIGFSLPMSIVAICYGLIAKIHKKMIKSSRPL 240
 Db 181 ASWGTPPEERLKVATMTLARGIIRFVIGFSLPMSIVAICYGLIAKIHKKMIKSSRPL 240

QY 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYGYKKIIDILVNPTSLAFNSCLNPM 300
 Db 241 RVLTAIVASFFICWPFQVALLGTWVKEMLFYGYKKIIDILVNPTSLAFNSCLNPM 300

QY 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDPAANSASPPAETELQAM 351
 Db 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDPAANSASPPAETELQAM 351

RESULT 9
 ADOS7846
 ID ADOS7846 standard; peptide; 351 AA.
 AC ADOS7846;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human formyl peptide receptor-like 1 SEQ ID NO:2.
 XX
 KW antiasthmatic; antiallergic; antiinflammatory; antiarteriosclerotic;
 KW neuroprotective; antiangiogenic; cerebroprotective; antiangiogenic; virtucide;
 KW antiinfective; immunomodulator; asthma; allergic disease; inflammation;
 KW arteriosclerosis; FPR1; formyl peptide receptor-like 1; human.
 XX
 OS Homo sapiens.
 OS
 PN WO2004041850-A1.
 XX
 PD 21-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-JP014138.
 XX
 PR 07-NOV-2002; 2002JP-00324189.
 PR 18-DEC-2002; 2002JP-00367119.
 PR 05-MAR-2003; 2003JP-00059073.
 PR 03-JUL-2003; 2003JP-00191359.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Hinuma S, Kobayashi M, Habata Y, Harada M, Okubo S, Yoshida H;
 PI Nishi K;
 XX

DR WPI; 2004-400641/37.
DR N-PSDB; AD057847.
XX
XX G protein-coupled receptor protein FPR1, its ligands, encoded
PT polynucleotides and antibodies for diagnosis and screening drugs
PT asthma, allergic diseases, inflammations and arteriosclerosis.
XX
PS Claim 25; SEQ ID NO 2; 191pp; Japanese.
XX
XX The invention relates to a novel peptide containing an amino acid
CC sequence identical or substantially similar to that of AD057845 or
CC AD057865 with 13 or 15 amino acids, respectively, in which the N-terminal
CC methionine is optionally formulated, its amide, ester or their salt. A
CC peptide of the invention has antiasthmatic, antiallergic,
CC antiinflammatory, antierosclerotic, neuroprotective, antianginal,
CC cerebroprotective, antinaemic, virucide, antinefective, and
CC immunomodulator activity. The receptor protein, its ligands, their
CC encoded polynucleotides and antibodies are useful in the diagnosis of and
CC screening drugs for e.g. asthma, allergic diseases, inflammations and
CC arteriosclerosis. With these ligands, agonists and antagonists can be
CC efficiently screened. An endogenous FPR1 (formyl peptide receptor-1) like
CC 1) ligand P3 was purified from pig's stomach after extraction and
CC chromatography for characterisation. Cloning of a rat spleen-originated
CC FPR1-encoded cDNA was also performed, and the clone was used in
CC constructing an expression vector and other biotechnological
CC manipulations as well as biological evaluation. The present sequence
CC represents human FPR1.
XX
SQ Sequence 351 AA:
Query Match 100.0%; Score 1817; DB 8; Length 351;
Best Local Similarity 100.0%; Pred. No. 7,8e-196;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 METNFSPLNMEYEEVSYESAGYVLRILPLVVGTVFVLGNGLVYVWAGFRMRTVT 60
DB 1 METNFSPLNMEYEEVSYESAGYVLRILPLVVGTVFVLGNGLVYVWAGFRMRTVT 60
QY 61 TICYNLALADFSFTATLPPLIVSMAMGEKMPGFLCKLIHVVDINLGSVFLGFIA 120
DB 61 TICYNLALADFSFTATLPPLIVSMAMGEKMPGFLCKLIHVVDINLGSVFLGFIA 120
QY 121 LDRICVLAHPVMAQNHRVSLAMKVIVGPWIALVLTLPVFLPTVTIPNGDYYCTFNF 180
DB 121 LDRICVLAHPVMAQNHRVSLAMKVIVGPWIALVLTLPVFLPTVTIPNGDYYCTFNF 180
QY 181 ASWGGTPEERLKAIVTMLTARGIIRVIGSLPMSIVAICGILAAKIHKKGMKSSRPL 240
DB 181 ASWGGTPEERLKAIVTMLTARGIIRVIGSLPMSIVAICGILAAKIHKKGMKSSRPL 240
QY 241 RVLTAAVASPFICWFPQVALAGTVMWKEMLFYKXKTIIDILVNPSSLAFFNSCLNPM 300
DB 241 RVLTAAVASPFICWFPQVALAGTVMWKEMLFYKXKTIIDILVNPSSLAFFNSCLNPM 300
QY 301 LYYFVGODPFRERLIHSLPTSLERALSDDSAPTNDTAAANSAPPAETELQAM 351
DB 301 LYYFVGODPFRERLIHSLPTSLERALSDDSAPTNDTAAANSAPPAETELQAM 351
RESULT 10
ADP24410
ID ADP24410 standard; protein; 351 AA.
XX
XX ADP24410;
XX
XX 18-NOV-2004 (first entry)
XX
XX PRO polypeptide SEQ ID NO:1588.
XX
XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW osteopathic; antidiabetic; dermatological; antipneumatic; antiallergic;
XX antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX

OS Unidentified.
XX
XX WO2004041170-A2.
XX
XX 21-MAY-2004.
XX
XX 30-OCT-2003; 2003WO-US034312.
XX
XX 01-NOV-2002; 2002US-0423394P.
XX
XX (GERTH) GENENTECH INC.
XX
XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
DR WPI; 2004-419628/39.
DR N-PSDB; ADP24409.
XX
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
XX Claim 7; SEQ ID NO 1588; 2940pp; English.
XX
XX The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipneumatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. A polynucleotide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.
XX
SQ Sequence 351 AA:
Query Match 100.0%; Score 1817; DB 8; Length 351;
Best Local Similarity 100.0%; Pred. No. 7,8e-196;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 METNFSPLNMEYEEVSYESAGYVLRILPLVVGTVFVLGNGLVYVWAGFRMRTVT 60
DB 1 METNFSPLNMEYEEVSYESAGYVLRILPLVVGTVFVLGNGLVYVWAGFRMRTVT 60
QY 61 TICYNLALADFSFTATLPPLIVSMAMGEKMPGFLCKLIHVVDINLGSVFLGFIA 120
DB 61 TICYNLALADFSFTATLPPLIVSMAMGEKMPGFLCKLIHVVDINLGSVFLGFIA 120
QY 121 LDRICVLAHPVMAQNHRVSLAMKVIVGPWIALVLTLPVFLPTVTIPNGDYYCTFNF 180
DB 121 LDRICVLAHPVMAQNHRVSLAMKVIVGPWIALVLTLPVFLPTVTIPNGDYYCTFNF 180
QY 181 ASWGGTPEERLKAIVTMLTARGIIRVIGSLPMSIVAICGILAAKIHKKGMKSSRPL 240
DB 181 ASWGGTPEERLKAIVTMLTARGIIRVIGSLPMSIVAICGILAAKIHKKGMKSSRPL 240

DB 181 ASWGTPBERLKYAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKMISRRPL 240
 QY 241 RVLTAIVASFFICWPFEPQVALLGTWMLKEMLPYGYKKIIDIIVNPTSSLAFNSCLNPM 300
 DB 241 RVLTAIVASFFICWPFEPQVALLGTWMLKEMLPYGYKKIIDIIVNPTSSLAFNSCLNPM 300
 QY 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDTAANSASPPAETELQAM 351
 DB 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDTAANSASPPAETELQAM 351

RESULT 11
 ADS74158
 ID ADS74158 standard; protein; 351 AA.
 AC ADS74158;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human LXA4 receptor.
 XX
 KM Human; Reso E receptor 1; LXA4; antiinflammatory;
 KM G-protein coupled receptor; receptor.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 122..142
 FT /note="Second intracellular loop"
 FT Domain 287..309
 FT /note="Transmembrane domain 7"
 XX
 PN MO2004078143-A2.
 XX
 PD 16-SEP-2004.
 XX
 PF 05-MAR-2004; 2004MO-US006766.
 XX
 PR 05-MAR-2003; 2003US-0452244P.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 XX
 PI Serhan CN, Arlta M;
 XX
 DR WPI; 2004-662347/64.
 XX
 PT Screening candidate substance for anti-inflammatory activity; involves
 PT connecting cell expressing Reso E receptor with candidate substance, and
 PT detecting biological activity mediated by Reso E receptor.
 XX
 PS Disclosure; Fig 3; 33pp; English.
 XX
 CC The present sequence is that of the human LXA4 receptor (ALX), a G-
 CC protein coupled receptor (GPCR). The invention is based, in part, on the
 CC recognition that resolvin E1 receptor (Reso E1) shares similar
 CC structural features to LO-derived eicosanoid receptors, such as the LXA4
 CC receptor. A claimed method of identifying a receptor that mediates an
 CC antiinflammatory activity of a resolvin substance comprises: introducing a
 CC nucleic acid configured to express a GPCR into a cell that does not
 CC endogenously produce the GPCR; contacting the cell with a substance
 CC comprising a resolvin; and detecting that the cell has a reduced cytokine
 CC induced activation of a NF-kB transcription factor relative to a cell not
 CC contacted by the substance. A claimed method for screening a candidate
 CC substance for antiinflammatory activity comprises detecting that the
 CC candidate substance alters an activity mediated by a GPCR. The GPCR
 CC preferably has sequence identity within the second intracellular loop or
 CC 7th transmembrane domain of human ALX.
 XX
 SQ Sequence 351 AA;
 Query Match 100.0%; Score 1817; DB 8; Length 351;
 Best Local Similarity 100.0%; Pred. No. 7,8e-196;
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFSPTLNEBYEVSBSAGTTVLRILPLVVLGTFVLGVLGNGLVIVAGFRMTRVYT 60
 DB 1 METNFSPTLNEBYEVSBSAGYTVLRILPLVVLGTFVLGVLGNGLVIVAGFRMTRVYT 60
 QY 61 TTYLNLALADPSFATLPLPLVSNMAGRKWPGMFLCKLHHVVDINLFGSVFLGLGFA 120
 DB 61 TTYLNLALADPSFATLPLPLVSNMAGRKWPGMFLCKLHHVVDINLFGSVFLGLGFA 120
 QY 121 LDRICVLHPVWAQNRRVTSLSAMKVIWGPWIIALVLTLPVPLFTVTIIPNGDYCTFNP 180
 DB 121 LDRICVLHPVWAQNRRVTSLSAMKVIWGPWIIALVLTLPVPLFTVTIIPNGDYCTFNP 180
 QY 181 ASWGTPBERLKYAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKMISRRPL 240
 DB 181 ASWGTPBERLKYAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKMISRRPL 240
 QY 241 RVLTAIVASFFICWPFEPQVALLGTWMLKEMLPYGYKKIIDIIVNPTSSLAFNSCLNPM 300
 DB 241 RVLTAIVASFFICWPFEPQVALLGTWMLKEMLPYGYKKIIDIIVNPTSSLAFNSCLNPM 300
 QY 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDTAANSASPPAETELQAM 351
 DB 301 LVYFVGQDFRERLIHSLPTSLERALSBDSPNTDTAANSASPPAETELQAM 351

RESULT 12
 ADX06859
 ID ADX06859 standard; protein; 351 AA.
 AC ADX06859;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 1424.
 XX
 KM cytostatic; cyclin-dependent kinase; cdk; biomarker.
 XX
 OS Homo sapiens.
 XX
 PN MO2005012875-A2.
 XX
 PD 10-FEB-2005.
 XX
 PF 29-JUL-2004; 2004MO-US024424.
 XX
 PR 29-JUL-2003; 2003US-0490890P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
 XX
 DR WPI; 2005-163068/17.
 XX
 PT Biomarkers useful for predicting or determining the response of a mammal
 PT to a cancer treatment comprising administration of a modulator of cyclin-
 PT dependent kinase activity.
 XX
 PS Claim 5; SEQ ID NO 1424; 141pp; English.
 XX
 CC This invention describes a novel method of predicting or determining
 CC whether a mammal will respond or is responding to an anti-cancer agent
 CC that modulates cyclin-dependent kinase (cdk) activity. The method
 CC comprises measuring the level of one or more biomarkers selected from
 CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
 CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
 CC invention is utilized in a kit for determining or predicting whether
 CC patient would be susceptible or resistant to treatment by an agent
 CC modulating cdk activity. The invention also describes a method for
 CC utilizing individualized genetic profiles for treating diseases and
 CC disorders based on patient's response and molecular level, specialized
 CC microarrays comprising the biomarkers described, antibodies directed

CC against the biomarkers and a cell culture model to identify biomarkers.
 CC The cdk modulator is preferably N-5-[(5-(1,1-Dimethyl-2-oxazolyl)methyl)thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
 CC tartaric acid salt. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences. This
 CC sequence represents a biomarker used in the method of the invention.

CC Sequence 351 AA;

Query Match 100.0%; Score 1817; DB 9; Length 351;

Best Local Similarity 100.0%; Pred. No. 7.8e-196;

Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNNEYEVESYBSAGYTVLRILPLVVLGVTFTVGLNGGLVIVWAGFRMTRTYT 60
 DB 1 METNFTPLNNEYEVESYBSAGYTVLRILPLVVLGVTFTVGLNGGLVIVWAGFRMTRTYT 60
 QY 61 TICYNLALADPSFTATLPFLIVSMAGKMPGFWFLCKLIHIVDINLFGSVFLIGFTA 120
 DB 61 TICYNLALADPSFTATLPFLIVSMAGKMPGFWFLCKLIHIVDINLFGSVFLIGFTA 120
 QY 121 LDRCTCVLHPWVAQNRRVTSLSMKYIVGPMIALVTLTPVFLTLTVTTPNGDTYCTFNF 180
 DB 121 LDRCTCVLHPWVAQNRRVTSLSMKYIVGPMIALVTLTPVFLTLTVTTPNGDTYCTFNF 180
 QY 181 ASWGTPEERLKVATITMLTARGIIRFVIGSLPMSIVAICYGLIAKHKKGIKSSRPL 240
 DB 181 ASWGTPEERLKVATITMLTARGIIRFVIGSLPMSIVAICYGLIAKHKKGIKSSRPL 240
 QY 241 RVLTAIVASFFICWPFQVALLGTWMLKEMLFYGYKXIIDLIVNPTSSLAFFNSCLNPM 300
 DB 241 RVLTAIVASFFICWPFQVALLGTWMLKEMLFYGYKXIIDLIVNPTSSLAFFNSCLNPM 300
 QY 301 LYFVQODFRERLIHSLPTSLRALSDSAPNTDPAANSAPPAETELQAM 351
 DB 301 LYFVQODFRERLIHSLPTSLRALSDSAPNTDPAANSAPPAETELQAM 351

RESULT 13

ID ADY73233 standard; protein; 351 AA.

XX AC ADY73233;

DT 02-JUN-2005 (first entry)

XX DE Human PPR1.

XX neuroprotective; nootropic; gene therapy; substrate inhibition;
 KW gene expression; diagnosis; Alzheimer's disease; neuroprotective;
 KW nootropic; degeneration; neurological disease; cognitive disorder; PPR1;
 KW receptor.

XX OS Homo sapiens.

XX PN W02005024057-A1.

XX PD 17-MAR-2005.

XX PF 10-SEP-2003; 2003WO-EP010160.

XX PR 10-SEP-2003; 2003WO-EP010160.

XX PA (GALA-) GALAPAGOS GENOMICS NV.

XX PI Merchiers PG, Splittels KF, Hoffmann M, Thyse K, Laenen W;

XX WPI; 2005-233298/24.

PT Identifying compound that changes amyloid beta precursor protein
 PT processing in cell; involves exposing cell to compound; comparing
 PT activity level of polypeptide before and after exposing cell to compound;

PT and identifying compound.

XX Example 2; Fig 8; 86pp; English.

XX The invention describes a method of identifying (M1) a compound that
 CC changes the amyloid-beta precursor protein processing in a cell,
 CC involving providing a host cell expressing a polypeptide having one of 14
 CC amino acid sequences (SEQ ID No. 15-28), determining activity level of
 CC polypeptide, exposing the host cell to a compound, determining activity
 CC level of the polypeptide, and identifying the compound, by which the
 CC second activity level is less than the first activity level. Also
 CC described are: changing the amyloid-beta precursor protein processing of
 CC a cell; a polynucleotide (I) comprising a nucleotide sequence chosen from
 CC one of 310 fully defined 21 base pair sequences (SEQ ID No. 29-318) given
 CC in the specification; a vector (II) comprising (I); and diagnosing a
 CC pathological condition involving cognitive impairment or a susceptibility
 CC to the condition in a subject. (M1) is useful for identifying a compound
 CC that changes the amyloid-beta precursor protein processing in a cell. (I)
 CC or (II) is useful as a medicament or for producing medicament for
 CC treating a disease (e.g. Alzheimer's disease) involving cognitive
 CC impairment. This is the amino acid sequence of human receptor PPR1
 CC associated with the reduction of GPCR expression and subsequent
 CC inhibition of amyloid beta production. Note: The invention claims SEQ ID
 CC No 8 1-28 which are not shown in the specification.

SQ Sequence 351 AA;

Query Match 100.0%; Score 1817; DB 9; Length 351;

Best Local Similarity 100.0%; Pred. No. 7.8e-196;

Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNNEYEVESYBSAGYTVLRILPLVVLGVTFTVGLNGGLVIVWAGFRMTRTYT 60
 DB 1 METNFTPLNNEYEVESYBSAGYTVLRILPLVVLGVTFTVGLNGGLVIVWAGFRMTRTYT 60
 QY 61 TICYNLALADPSFTATLPFLIVSMAGKMPGFWFLCKLIHIVDINLFGSVFLIGFTA 120
 DB 61 TICYNLALADPSFTATLPFLIVSMAGKMPGFWFLCKLIHIVDINLFGSVFLIGFTA 120
 QY 121 LDRCTCVLHPWVAQNRRVTSLSMKYIVGPMIALVTLTPVFLTLTVTTPNGDTYCTFNF 180
 DB 121 LDRCTCVLHPWVAQNRRVTSLSMKYIVGPMIALVTLTPVFLTLTVTTPNGDTYCTFNF 180
 QY 181 ASWGTPEERLKVATITMLTARGIIRFVIGSLPMSIVAICYGLIAKHKKGIKSSRPL 240
 DB 181 ASWGTPEERLKVATITMLTARGIIRFVIGSLPMSIVAICYGLIAKHKKGIKSSRPL 240
 QY 241 RVLTAIVASFFICWPFQVALLGTWMLKEMLFYGYKXIIDLIVNPTSSLAFFNSCLNPM 300
 DB 241 RVLTAIVASFFICWPFQVALLGTWMLKEMLFYGYKXIIDLIVNPTSSLAFFNSCLNPM 300
 QY 301 LYFVQODFRERLIHSLPTSLRALSDSAPNTDPAANSAPPAETELQAM 351
 DB 301 LYFVQODFRERLIHSLPTSLRALSDSAPNTDPAANSAPPAETELQAM 351

RESULT 14

ID AEA27939 standard; protein; 351 AA.

XX AC AEA27939;

DT 28-JUL-2005 (first entry)

XX DE Human formyl peptide receptor-like 1.

XX Formyl peptide receptor-like 1; Lipoxin A4 receptor;
 KW rheumatoid arthritis; immune disorder; inflammation;
 KW musculoskeletal disease; antiarthritic; antiinflammatory;
 KW Alzheimer's disease; neurological disease; degeneration; nootropic;
 KW neuroprotective; asthma; antiaesthetic; respiratory disease; trauma;
 KW vulnerability; injury; radiation injury; autonomic; cytostatic;
 KW renal disease; nephrotropic; endocrine disease; genitourinary disease;

glomerular disease; cardiovascular disease; hypertension; hypotensive;
myocardial infarction; cardiome; myocardial ischemia; vasotropic;
allergy; antiallergic; immune disorder; shock; gout; antigout;
musculoskeletal disease; psoriasis; antipsoriatic;
dermatological disease; allergic; rhinitis; ear; nose; throat disease;
respiratory distress syndrome; respiratory-gen.; respiratory disease;
Crohn's disease; gastroenteric shock; gastrointestinal disease;
hemorrhagic shock; endotoxic shock; glomerular disease;
benign prostatic hypertrophy; neoplasm; inflammatory bowel disease;
brain injury; cerebroprotective; systemic lupus erythematosus;
metabolic disorder; vasoconstriction; pain; analgesic; diabetes;
antidiabetic; bacterial infection; antibacterial; viral infection;
viricide; cancer.

Homo sapiens.
MO2005047899-A2.

26-MAY-2005.

04-NOV-2004; 2004MO-US036952.

07-NOV-2003; 2003US-0518476P.
10-NOV-2003; 2003US-0519085P.
30-JUL-2004; 2004US-0592926P.

(ACAD-) ACADIA PHARM INC.

Nash N, Scully AL, Gardell L, Olsson R, Gustafsson M;
WPI, 2005-395823/40.
N-PSDB; AEA27938.

Use of lipoxin receptor as screening tool to identify compounds effective
in treating inflammation and associated pain.

Claim 5; SEQ ID NO 2; 75bp; English.

The present sequence is the protein sequence of human formyl peptide
receptor-like 1 (FPR1), also known as lipoxin A4 receptor. The invention
relates to the use of the FPR1 as a tool to identify compounds effective
in treating inflammation and associated pain, and to the use of such
compounds as therapeutics. A method of screening for a compound able to
affect one or more activities of a FPR1 receptor comprises: (a)
contacting a recombinant cell with a test compound, where the recombinant
cell comprises a recombinant nucleic acid expressing FPR1 (provided the
cell does not have endogenous FPR1 expression); and (b) determining the
ability of the test compound to affect one or more activities of FPR1. A
compound that activates a FPR1 receptor subtype is used in a claimed
method for treating acute and chronic inflammation, such as inflammation
associated with diabetes, viral infection, irritable bowel syndrome,
amputation, cancer, bacterial infection, physical injury, including
physical trauma and radiation exposure, vasoconstriction as a result of
asthma, anaphylactic reactions, allergic reactions, shock, diabetes,
rheumatoid arthritis, gout, psoriasis, allergic rhinitis, adult
respiratory distress syndrome, Crohn's disease, endotoxin shock,
traumatic shock, hemorrhagic shock, bowel ischemic shock, renal
glomerular disease, benign prostatic hypertrophy, myocardial ischemia,
myocardial infarction, circulatory shock, brain injury including ischemic
stroke and hemorrhagic stroke, systemic lupus erythematosus, chronic
renal disease, cardiovascular disease and hypertension or chemical injury
(all claimed). Also claimed are: cells that express FPR1 receptor, which
are used in a claimed method of identifying agonists of FPR1; a method
of treating inflammation, where the inflammatory response results from
the activation of leukocytes and comprises leukocyte migration and
generation of reactive oxygen species to evoke vascular leakage or edema,
is associated with rheumatoid arthritis, Alzheimer's disease or asthma,
results from physical injury, including physical trauma and radiation
exposure; a method of inducing vasodilation to treat or prevent a
vasoconstrictive response or condition such as renal hemodynamic disease,
including glomerular disease, a cardiovascular disease including
hypertension, myocardial infarction and myocardial ischemia; and a method
for antagonizing a vasoconstrictive response to a endothelide

CC leukotriene in a subject, where the response is a renal vasoconstrictive
CC response including mild vasoconstriction such as chronic renal disease
CC and chronic severe vasoconstriction such as glomerular kidney disease.
XX

XX Sequence 351 AA;
SQ

Query Match 100.0%; Score 1817; DB 9; Length 351;
Best Local Similarity 100.0%; Pred. No. 7.8e-196;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNXYEVEYSEYSGYTVLRILPLVYLVGVTVGVNGLVVWAGFRMRTVT 60
DB 1 METNFTPLNXYEVEYSEYSGYTVLRILPLVYLVGVTVGVNGLVVWAGFRMRTVT 60

QY 61 TICYNLALADSPFTATLPLVYVMAWGEKWPGEFLCTLIHIVVDINFGSVFLGFIA 120
DB 61 TICYNLALADSPFTATLPLVYVMAWGEKWPGEFLCTLIHIVVDINFGSVFLGFIA 120

QY 121 LDRCTCVLHPVMAQNHRTVSLAMKVYGVWIIALVTLTPEVFLPTVTTPNGDTYCTENF 180
DB 121 LDRCTCVLHPVMAQNHRTVSLAMKVYGVWIIALVTLTPEVFLPTVTTPNGDTYCTENF 180

QY 181 ASWGTPEERLKVATIMLTARAGIIRPVIGPSLPMSTVATCYGLIAKHKKGIKSSRPL 240
DB 181 ASWGTPEERLKVATIMLTARAGIIRPVIGPSLPMSTVATCYGLIAKHKKGIKSSRPL 240

QY 241 RVLTAIVASFFLCWPEPQVALIGTVMLKEMLFYGYKIIIDILVNPTSSLAFFNSCLNPM 300
DB 241 RVLTAIVASFFLCWPEPQVALIGTVMLKEMLFYGYKIIIDILVNPTSSLAFFNSCLNPM 300

QY 301 LVYVQGDPRERLIHSLPTSLERALSBDSPAPNDPAANSASPAPTELOAM 351
DB 301 LVYVQGDPRERLIHSLPTSLERALSBDSPAPNDPAANSASPAPTELOAM 351

RESULT 15
ABU10071
ID ABU10071 standard; protein; 370 AA.
XX
AC ABU10071;
XX
DT 15-AUG-2003 (first entry)
XX
XX Human G-protein coupled receptor HGPBMY39.
DE
XX Human; receptor; G-protein coupled receptor; HGPBMY39; cancer;
KW male reproductive disorder; developmental disorder; immune disorder;
KW inflammatory disorder; testicular cancer; leukemia;
KW bone marrow disorder; testicular cancer; proliferative disorder;
KW neural disorder; Alzheimer's disease; prion disorder;
KW bone metabolism disorder.
XX
OS Homo sapiens.
XX
EH Key Location/Qualifiers
FT Region 2..370
FT /note= "This region is claimed in claim 5"
XX
PN MO2003023007-A2.
XX
XX 20-MAR-2003.
PD
XX 06-SEP-2002; 2002WO-US028582.
PF
XX 07-SEP-2001; 2001US-0317793P.
PR
XX 27-NOV-2001; 2001US-0333658P.
PR
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA
XX Ramanathan CS, Gopal S, Mintler G, Feder JN;
PI WPI, 2003-313245/30.
XX
DR N-PSDB; ACA61401.

XX New human G-protein coupled receptor, HGPBMY39, useful for treating or
PT preventing e.g. immune, inflammatory, developmental, proliferative,
PA neural, reproductive, bone marrow or prion disorders.

PS Claim 5; Fig 1; 359pp; English.

XX The invention relates to an isolated nucleic acid encoding a human G-
CC protein coupled receptor HGPBMY39 (or its fragment domain or epitope),
CC its complement or a polynucleotide capable of hybridising under stringent
CC conditions to it. Also included are a HGPBMY39 recombinant vector, a
CC recombinant host cell comprising the vector sequences (used to express
CC and make the protein), an isolated HGPBMY39 polypeptide, and an anti-
CC HGPBMY39 antibody. The HGPBMY39 polynucleotides and polypeptide is
CC useful for preventing, treating or ameliorating e.g. a (male)
CC reproductive disorder; a testicular disorder or cancer; a disorder
CC related to aberrant G-protein coupled signalling, particularly N-formyl
CC peptide receptor dependent signalling; a disorder related to aberrant G-
CC protein coupled receptor dependent phosphatidylinositol-calcium
CC signalling; a disorder related to aberrant G-protein couple receptor
CC dependent phosphatidylinositol or calcium second messenger activation; an
CC immune disorder; an inflammatory disorder; a developmental disorder; a
CC disorder that would benefit from inhibition of a leukotriene B4-dependent
CC proinflammatory signal; aberrant N-formyl peptide signalling; aberrant
CC neutrophil activation; a disorder associated with hyper neutrophil
CC activation; a disorder associated with below normal neutrophil activation
CC ; a disorder related to aberrant intracellular and/or extracellular
CC oxidation states; a disorder related to aberrant superoxide generation;
CC leukaemia; a bone marrow disorder; cancer; proliferative disorders;
CC neural disorders; a disorder related to aberrant neutrophil chemotaxis;
CC Alzheimer's disease; prion disorders; and a bone metabolism disorder. The
CC present sequence represents HGPBMY39

XX
SQ Sequence 370 AA;

Query Match 100.0%; Score 1817; DB 6; Length 370;
Best Local Similarity 100.0%; Pred. No. 8.4e-196;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFSPTLNEYREVSYESAGYTLRLPLVVLGVTVLGVNGGLVYVWAGFRMTRTVT 60
DB 20 METNFSPTLNEYREVSYESAGYTLRLPLVVLGVTVLGVNGGLVYVWAGFRMTRTVT 79
QY 61 TICVNLALADSPFTATLPFLIVSMANGKMPFCMPLCKLIHIVVDINLFGSVFLIGFIA 120
DB 80 TICVNLALADSPFTATLPFLIVSMANGKMPFCMPLCKLIHIVVDINLFGSVFLIGFIA 139
QY 121 LDRICVLAHPVMAQNRTVSLAMKVIQVPIALVLTLPVFLPTVTINPGDYCTENF 180
DB 140 LDRICVLAHPVMAQNRTVSLAMKVIQVPIALVLTLPVFLPTVTINPGDYCTENF 199
QY 181 ASWGGTPEERLKAIVTMTLARGIIRFYIGSLPMSIYACGLIAAKIHKKGMIKSRPL 240
DB 200 ASWGGTPEERLKAIVTMTLARGIIRFYIGSLPMSIYACGLIAAKIHKKGMIKSRPL 259
QY 241 RVLTAIVASFFICMFPFQVALLGTWVKEMLPYKGYKIIDIIVNPSSLAFFNSCLNPM 300
DB 260 RVLTAIVASFFICMFPFQVALLGTWVKEMLPYKGYKIIDIIVNPSSLAFFNSCLNPM 319
QY 301 LYYFVGQDFRERLIHSLPTSLERALSBSAFTNDTANASAPPAETELQAM 351
DB 320 LYYFVGQDFRERLIHSLPTSLERALSBSAFTNDTANASAPPAETELQAM 370

Search completed: March 28, 2006, 13:14:57
Job time : 254.22 secs

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* OM protein - protein search, using sw model

Run on: March 28, 2006, 13:10:18 ; Search time 17.28 Seconds
(without alignments)
610.248 Million cell updates/sec

Title: US-10-517-956-3

Perfect score: 120
Sequence: 1 MAPRGFSCLLLTSEIDLVRKRA 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seque, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	24	4 AAB73993	Aab73993 Human HN
2	120	100.0	24	4 AAB81835	Aab81835 Nerve cel
3	120	100.0	24	5 ABB44628	Abb44628 Human pro
4	120	100.0	24	5 AAU73274	Aau73274 Human pro
5	120	100.0	24	5 AAU69614	Aau69614 Cell deat
6	120	100.0	24	6 AAO30161	Aao30161 Human hum
7	120	100.0	24	7 AAO30314	Aao30314 Human hum
8	120	100.0	24	8 ADF95055	Adf95055 Humanin p
9	120	100.0	24	8 ADF95059	Adf95059 Humanin p
10	120	100.0	24	8 ADF95060	Adf95060 Humanin p
11	120	100.0	24	8 ADF95052	Adf95052 Humanin p
12	120	100.0	24	8 ADF95057	Adf95057 Humanin p
13	120	100.0	24	8 ADF95056	Adf95056 Humanin p
14	120	100.0	24	8 ADF95078	Adf95078 Humanin p
15	120	100.0	24	8 ADF95058	Adf95058 Humanin p
16	120	100.0	24	8 ADH58977	Adh58977 Human GPC
17	120	100.0	24	8 ADH53325	Adh53325 Human hum
18	120	100.0	24	8 ADO80239	Ado80239 Modified
19	120	100.0	24	8 ADS64578	Ads64578 Human hum
20	120	100.0	24	9 AEA23775	Aea23775 Human PRO
21	120	100.0	24	9 AEB06773	Aeb06773 Nephrotic
22	120	100.0	32	8 ADF95068	Adf95068 Humanin p
23	120	100.0	34	4 AAB73994	Aab73994 Human SHN
24	120	100.0	34	4 AAB81836	Aab81836 Nerve cel

25	117	97.5	24	8 ADF95063	Adf95063 Humanin p
26	117	97.5	32	8 ADF95066	Adf95066 Humanin p
27	116	96.7	24	4 AAB73995	Aab73995 Human HN
28	116	96.7	24	4 AAB81838	Aab81838 Nerve cel
29	116	96.7	24	8 ADF95053	Adf95053 Humanin p
30	116	96.7	24	8 ADH58978	Adh58978 Human GPC
31	116	96.7	24	8 ADF53326	Adf53326 Human hum
32	116	96.7	32	8 ADF95070	Adf95070 Humanin p
33	115	95.8	23	4 AAB81841	Aab81841 Nerve cel
34	114	95.0	24	4 AAB81837	Aab81837 Nerve cel
35	111	92.5	22	4 AAB81842	Aab81842 Nerve cel
36	111	92.5	24	4 AAB73996	Aab73996 Human HN
37	111	92.5	24	4 AAB81839	Aab81839 Nerve cel
38	111	92.5	24	7 AAO30329	Aao30329 Human hum
39	111	92.5	24	8 ADF95054	Adf95054 Humanin p
40	111	92.5	32	8 ADF95069	Adf95069 Humanin p
41	106	88.3	21	8 ADH58980	Adh58980 Human GPC
42	106	88.3	21	8 ADI53327	Adi53327 Human hum
43	106	88.3	24	4 AAB81879	Aab81879 Nerve cel
44	106	88.3	24	4 AAB81886	Aab81886 Nerve cel
45	106	88.3	24	4 AAB81876	Aab81876 Nerve cel

ALIGNMENTS

RESULT 1
AAB73993
ID AAB73993 standard; peptide; 24 AA.
AC AAB73993;
DT 12-JUN-2001 (first entry)
XX
DE Human HN peptide.
XX
XX Human; disease inhibiting gene; gene screening; protein screening;
XX drug identification; gene therapy; cell-death associated disease;
XX central nervous system disorder; Alzheimer's disease;
XX Huntington's disease; cerebrospinal ataxia; apoptosis;
XX familial amyotrophic lateral sclerosis; HN.
XX Homo sapiens.
XX
XX
XX WO200121786-A1.
XX
XX
XX 29-MAR-2001.
XX
XX 14-SEP-2000; 2000WO-JP006313.
XX
XX 17-SEP-1999; 99JP-00264679.
XX 29-JUN-2000; 2000JP-00201456.
XX
XX (UYKE-) UNIV KEIO.
XX
XX Nishimoto I;
XX
XX WPI; 2001-257964/26.
XX N-PSDB; AAF82222.
XX
XX Screening for disease inhibiting genes and peptides for treatment of
XX nervous system diseases involving cell death.
XX
XX Example 2; Page 37; 75pp; Japanese.
XX
XX The present sequence is provided in a specification relating to a method
XX for screening for disease inhibiting genes and peptides. Nucleic acids
XX originating in cells from patients suffering from the disease are
XX introduced into a host cell and expressed in that cell, the effect on
XX cell death is determined, and nucleic acids are selected in which a
XX depressant effect on cell death is observed. The method is useful in the
XX identification of drugs for treatment and gene therapy of cell-death
XX associated diseases of the central nervous system, such as Alzheimer's

CC disease, Huntington's disease, cerebrospinal ataxia and familial
CC amyotrophic lateral sclerosis
XX
SQ Sequence 24 AA;

Query Match 100.0%; Score 120; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPRGSCLLLTSEIDL PVKRRR 24
DB 1 MAPRGSCLLLTSEIDL PVKRRR 24

RESULT 2
AAB81835
ID AAB81835 standard; peptide; 24 AA.

AC AAB81835;
DT 06-JUN-2001 (first entry)

DE Nerve cell death inhibition method related peptide SEQ ID NO: 5.

XX Alzheimer's disease; nerve cell death; APP variant; presenilin variant;
KM humanin.

XX Homo sapiens.

OS WO200121787-A1.

XX 29-MAR-2001.

XX 14-SEP-2000; 2000MO-JF006314.

XX 17-SEP-1999; 99JP-00264679.

PR 29-JUN-2000; 2000JP-00201456.

XX (UYKE-) UNIV KEIO.

XX Nishimoto I;

DR WPI; 2001-290433/30.

DR N-PSDB; AAF81621.

XX Humanin peptides which inhibits cell death useful for treatment of

PT Alzheimer's and other nervous system diseases.

XX Example 1; Page 94; 116pp; Japanese.

XX The present invention provides humanin peptides which inhibit cell death

CC associated with Alzheimer's disease. They can be used in the treatment of

CC Alzheimer's disease and as models for the development of new drugs useful

CC in treating the same

XX Sequence 24 AA;

SQ

Query Match 100.0%; Score 120; DB 4; Length 24;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPRGSCLLLTSEIDL PVKRRR 24

DB 1 MAPRGSCLLLTSEIDL PVKRRR 24

RESULT 3

ABBA4628

ID ABBA4628 standard; peptide; 24 AA.

XX

AC ABBA4628;

XX

DT 07-FEB-2002 (first entry)

XX Human protective sequence CNI-00734 peptide #5.

DE Human; protective sequence; cell death; cancer; autoimmune disease;
XX neurologi disorder; stroke; cytostatic; neuroprotective; gene therapy.

XX Homo sapiens.

OS WO200176457-A2.

XX 18-OCT-2001.

XX 09-APR-2001; 2001MO-US011663.

XX 11-APR-2000; 2000US-00547735.

XX (COGE-) COCENT NEUROSCIENCE INC.

PA Thomas MB, Portbury SD, Puranam K, Katz LC, Lo DC, Barney S;

PI WPI; 2002-025874/03.

DR N-PSDB; ABA82707.

XX New protective sequences and their products, useful for diagnosing and

PT treating diseases involving cell death, including neurological disorders

PT e.g. stroke and for identifying modulators of expression of the

PT protective sequences.

XX Claim 1; Fig 4; 283pp; English.

XX The present invention relates to protective sequence proteins (ABBA4624-

CC ABA84830) and their coding sequences (ABA82701-ABA82937). The sequences,

CC when introduced into a cell either predisposed to undergo cell death or

CC in the process of undergoing cell death, prevent, delay or rescue the

CC cell from death, hence, these sequences are named "protective sequences".

CC The sequences are useful for treating and/or ameliorating cancer.

CC autoimmune diseases and neurological disorders e.g. stroke. Further

CC examples of diseases which may be treated by the present invention are

CC given in the specification

XX Sequence 24 AA;

SQ

Query Match 100.0%; Score 120; DB 5; Length 24;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPRGSCLLLTSEIDL PVKRRR 24

DB 1 MAPRGSCLLLTSEIDL PVKRRR 24

RESULT 4

AU73274

ID AU73274 standard; peptide; 24 AA.

XX 12-MAR-2002 (first entry)

XX Human protective DNA sequence CNI-00736 open reading frame #5.

XX Human; protective sequence; cell death; central nervous system; stroke;

XX ischaemia; open reading frame; ORF; cerebral herniation; septic embolism;

XX cerebral oedema; meningitis; protozoal infection; malaria; CNI-00733;

XX metazoal infection; vascular disease; eye; macular degeneration; trauma;

XX diabetic retinopathy; epidural haematoma; tumour; degenerative disease;

XX nutritional condition; environmental condition; metabolic condition;

XX CNI-00736; CNI-00738; CNI-00742; CNI-00748; cancer; gene therapy.

XX Homo sapiens.

OS WO200181361-A1.

XX

PN

XX

PD 01-NOV-2001.
 XX
 XX 09-APR-2001; 2001WO-US011501.
 XX
 XX 11-APR-2000; 2000US-00547938.
 XX
 PA (COGE-) COGENT NEUROSCIENCE INC.
 XX
 XX Portbury SD, Puranam K, Katz LC, Lo DC, Barney S, Thomas MB;
 XX
 DR WPI; 2002-066433/09.
 DR N-PSDB; AAS98431.
 XX
 XX Polypeptides and polynucleotides comprising protective sequences useful
 PT for preventing, delaying or rescuing a cell from death in disease,
 PT condition or disorders such as Alzheimer's disease, stroke, tumors,
 PT trauma.
 XX
 XX Claim 17, Fig 5F; 228pp; English.
 XX
 XX The invention relates to an isolated polypeptide encoded by a protective
 CC sequence, which is a polynucleotide comprising sequences which, when
 CC introduced into a cell either predisposed to undergo cell death or in the
 CC process of undergoing cell death, prevent, delay, or rescue the cell from
 CC death, relative to a corresponding cell into which exogenous nucleic
 CC acids have been introduced. The sequences of the invention are useful for
 CC diagnosing a protective sequence-mediated condition, disorder or disease
 CC in an individual. The treatable disorders are preferably of the central
 CC nervous system of humans including ischemia-related conditions such as
 CC stroke, cerebral herniation, septic embolism, cerebral oedema, infections
 CC such as meningitis, protozoal infections such as malaria, metazoal
 CC infections such as echinococcosis, vascular diseases such as ischemic
 CC encephalopathy, conditions involving the eye such as macular
 CC degeneration, diabetic retinopathy, trauma such as epidural haematoma,
 CC tumours such as primary intracranial tumours, degenerative diseases such
 CC as Alzheimer's disease and nutritional, environmental and metabolic
 CC conditions. Sequences AAU7325-AAU7378 represent open reading frames of
 CC the human protective sequence polynucleotides
 XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 120; DB 5; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MARRGFSCLLLTSEIDLPVKRR 24
 1 MARRGFSCLLLTSEIDLPVKRR 24
 Db
 RESULT 5
 AAU69614
 ID AAU69614 standard; protein; 24 AA.
 XX
 AC AAU69614;
 XX
 DT 30-JAN-2002 (first entry)
 XX
 XX Cell death protective sequence CNI-00725, protein #4.
 XX
 XX Human; protective sequence; cell death; cerebral oedema; infection;
 KM meningitis; degenerative disease; Alzheimer's disease; heart disease;
 KM motor neuron disease; demyelinating disease; multiple sclerosis; asthma;
 KM nutritional condition; peripheral nervous system disorder; ischaemia;
 KM diabetic neuropathy; autoimmune haemolytic anaemia; respiratory system;
 KM oral cavity; gastrointestinal tract; liver; cirrhosis; pancreatitis;
 KM polycystic renal disease; urinary tract; genitalia; endometriosis;
 KM breast; chronic mastitis; thyroid gland; Hashimoto's thyroiditis;
 KM adrenal gland; skin; psoriasis; muscular atrophy; bone marrow;
 KM osteoporosis; cancer; autoimmune disease.
 XX
 XX Homo sapiens.
 XX

PN W0200176532-A2.
 XX
 XX 18-OCT-2001.
 PD
 XX 09-APR-2001; 2001WO-US011655.
 PE
 XX 11-APR-2000; 2000US-00547596.
 XX
 PA (COGE-) COGENT NEUROSCIENCE INC.
 XX
 XX Portbury SD, Puranam K, Katz LC, Lo DC;
 XX
 DR WPI; 2002-017408/02.
 DR N-PSDB; AAS63013.
 XX
 XX Novel nucleic acids referred as protective sequences and their encoded
 PT products for diagnosing, treating diseases involving cell death,
 PT including neurological disorders e.g. stroke and for identifying
 PT modulators.
 XX
 XX Claim 17, Fig 6D; 256pp; English.
 XX
 XX The invention relates to isolated protective sequence polypeptides (I)
 CC and polynucleotides (II). (II) is useful for transferring a protective
 CC sequence into a cell, which delays and/or prevents the cell from
 CC undergoing cell death. Protective sequences, their products or antibodies
 CC are useful diagnostically, prophylactically, therapeutically or as
 CC targets for treatment and diagnosis of conditions, disorders or diseases
 CC involving cell death. The protective sequences and their products are
 CC useful for preventing or treating disorders of the central nervous system
 CC including neurological and psychiatric conditions, cerebral oedema,
 CC infections such as meningitis, degenerative diseases such as Alzheimer's
 CC and motor neuron disease, demyelinating diseases such as multiple
 CC sclerosis, nutritional conditions, disorders of the peripheral nervous
 CC system including diabetic neuropathy, disorders which cause cell death in
 CC organ systems including blood vessels, heart (ischaemia), blood cells
 CC (autoimmune haemolytic anaemia), respiratory system (asthma), oral
 CC cavity, gastrointestinal tract, liver (cirrhosis), pancreatitis,
 CC polycystic renal disease, urinary tract, genitalia (congenital
 CC anomalies), endometriosis, breast (chronic mastitis), thyroid gland
 CC (Hashimoto's thyroiditis), adrenal gland, skin (psoriasis)
 CC musculoskeletal system (muscular atrophy), bone marrow or bone
 CC (osteoporosis). The compositions promote cell death and are useful for
 CC treating and/or ameliorating cancer and autoimmune diseases. The
 CC compounds are further useful for treating physiological impacts on organs
 CC caused by infection which induce cell death. (I) is useful to raise an
 CC immune response, as a reagent in assays designed to quantitatively
 CC determine levels of the protein in biological fluids, as markers for
 CC tissues in which the corresponding protein is expressed and to isolate
 CC polypeptide sequences as described in the invention
 XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 120; DB 5; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MARRGFSCLLLTSEIDLPVKRR 24
 1 MARRGFSCLLLTSEIDLPVKRR 24
 Db
 RESULT 6
 AA030161
 ID AA030161 standard; peptide; 24 AA.
 XX
 AC AA030161;
 XX
 DT 03-SEP-2003 (first entry)
 XX
 XX Human humanin protein, HNL.
 XX

KM Human; aging-associated disease; oxidative stress; AAD; HNL; humanin.
 XX
 XX Homo sapiens.
 OS
 XX WO2003045988-A2.
 PN
 XX 05-JUN-2003.
 PD
 XX
 XX 28-NOV-2002; 2002WO-EP013549.
 PF
 XX 29-NOV-2001; 2001EP-00204600.
 PR
 XX (VLA-) VLAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 PA
 XX Contreras RH, Chen C;
 PI
 XX WPI; 2003-505183/47.
 DR
 XX N-PSDB; AAL60805.
 PT
 XX Screening genes involved in aging and/or aging-associated diseases or in
 PT oxidative stress by mutating and cultivating a yeast cell, enriching the
 PT population, labeling the mother cells and isolating the highly labeled
 PT cells.
 PS
 XX Claim 13; Page 38; 78pp; English.
 CC
 XX The invention relates to a method for screening genes involved in aging
 CC and/or aging-associated diseases (AAD) or in oxidative stress. The method
 CC involves mutating and cultivating a yeast cell, enriching the population
 CC for mother cells, labeling the mother cells and isolating the highly
 CC labelled cells. The present sequence is human humanin protein, HNL. This
 CC sequence is used to illustrate the method of the invention
 CC
 XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 120; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPRGFSCLLLTSEIDLPVKRRR 24
 Db 1 MAPRGFSCLLLTSEIDLPVKRRR 24
 RESULT 7
 AAO30314
 ID AAO30314 standard; peptide; 24 AA.
 XX
 AC AAO30314;
 XX
 DT 22-SEP-2003 (first entry)
 DE Human humanin (cytosolic form) peptide.
 XX
 XX Humanin; bax; bid; therapy; Alzheimer's disease; Parkinson's disease;
 KM neuron cell death; cancer; autoimmune disorder; nootropic; vasotrophic;
 KM anticonvulsant; tranquilizer; vulnery; cardiac; antiinflammatory;
 KM stroke; Huntington's disease; trauma; amyotrophic lateral sclerosis;
 KM human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003046205-A2.
 XX
 PD 05-JUN-2003.
 XX
 PF 27-NOV-2002; 2002WO-US038191.
 PR 28-NOV-2001; 2001US-0334149P.
 PA (BURN-) BURNHAM INST.
 XX
 XX Reed JC, Guo B;
 PI

XX WPI; 2003-505209/47.
 DR N-PSDB; AAL61053.
 XX
 XX Identifying modulators of apoptosis, in particular binding modulators of
 PT humanin to bax or bid, useful for diagnosing and/or treating disorders
 PT such as Alzheimer's disease, Parkinson's disease, cancer and inflammatory
 PT disorders.
 XX
 XX Disclosure; Fig 3B; 141pp; English.
 PS
 XX
 CC The invention relates to method for identifying an effective compound
 CC that modulates the binding of humanin to bax and/or bid. The method is
 CC useful for diagnosing and/or treating disorders associated with the
 CC humanin-bax or humanin-bid complex, such as Alzheimer's disease, stroke,
 CC Parkinson's disease, Huntington's disease, trauma, amyotrophic lateral
 CC sclerosis, neuron cell death, cancer or inflammatory or autoimmune
 CC disorders. The present sequence is human humanin (cytosolic form)
 CC peptide. This sequence is used to illustrate the method of the invention
 CC
 XX
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 120; DB 7; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPRGFSCLLLTSEIDLPVKRRR 24
 Db 1 MAPRGFSCLLLTSEIDLPVKRRR 24
 RESULT 8
 ADF95055
 ID ADF95055 standard; peptide; 24 AA.
 XX
 AC ADF95055;
 XX
 DT 26-FEB-2004 (first entry)
 DE Humanin peptide derivative P-S14 HN.
 XX
 XX HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;
 KM Alzheimer's disease.
 KM
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 14 /note="phosphorylated"
 FT
 PN WO2003097687-A2.
 XX
 PD 27-NOV-2003.
 XX
 PF 16-MAY-2003; 2003WO-JP006139.
 PR 16-MAY-2002; 2002US-0380958P.
 XX
 XX (NISH/) NISHIMOTO I.
 PA
 XX Nishimoto I;
 PT
 DR WPI; 2004-061983/06.
 XX
 PT New Humanin derivative that protects a neuronal cell from cytotoxicity,
 PT useful for treating neurodegenerative disorders (e.g. Alzheimer's
 PT disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated
 PT amino acid.
 XX
 PS Claim 8; SEQ ID NO 4; 82pp; English.
 XX
 CC The invention relates to a derivative of humanin (HN) that protects a

CC neuronal cell from cytotoxicity, where the derivative contains at least
CC one D-amino acid or phosphorylated amino acid, or where the derivative
CC has an addition of one or more amino acids having an activity of forming
CC a multimer. The humanin derivatives are useful in protecting neuronal
CC cells from cytotoxicity related to neurodegenerative diseases. The
CC composition and method are useful in treating neurodegenerative
CC disorders, such as Alzheimer's disease. The present sequence represents a
CC HN peptide derivative.
XX
SQ Sequence 24 AA;
Query Match 100.0%; Score 120; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPRGFSCLLLTSEIDLVPVGRRA 24
1 MAPRGFSCLLLTSEIDLVPVGRRA 24
Db 1 MAPRGFSCLLLTSEIDLVPVGRRA 24
RESULT 9
ADP95059
ID ADP95059 standard; peptide: 24 AA.
AC ADF95059;
XX 26-FEB-2004 (first entry)
XX
XX Humanin peptide derivative D-Ser7 HN.
XX HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;
XX Alzheimer's disease.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 7
XX /note= "D-form residue"
XX
XX WO2003097687-A2.
XX
XX 27-NOV-2003.
XX
XX 16-MAY-2003; 2003WO-JP006139.
XX
XX 16-MAY-2002; 2002US-0380958P.
XX
XX (NISH/) NISHIMOTO I.
XX
XX Nishimoto I;
XX
XX WPI; 2004-061983/06.
XX
XX New Humanin derivative that protects a neuronal cell from cytotoxicity,
XX useful for treating neurodegenerative disorders (e.g. Alzheimer's
XX disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated
XX amino acid.
XX
XX Claim 8; SEQ ID NO 8; 82pp; English.
XX
XX The invention relates to a derivative of humanin (HN) that protects a
XX neuronal cell from cytotoxicity, where the derivative contains at least
XX one D-amino acid or phosphorylated amino acid, or where the derivative
XX has an addition of one or more amino acids having an activity of forming
XX a multimer. The humanin derivatives are useful in protecting neuronal
XX cells from cytotoxicity related to neurodegenerative diseases. The
XX composition and method are useful in treating neurodegenerative
XX disorders, such as Alzheimer's disease. The present sequence represents a
XX HN peptide derivative.
XX
SQ Sequence 24 AA;

Query Match 100.0%; Score 120; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPRGFSCLLLTSEIDLVPVGRRA 24
1 MAPRGFSCLLLTSEIDLVPVGRRA 24
Db 1 MAPRGFSCLLLTSEIDLVPVGRRA 24
RESULT 10
ADP95060
ID ADP95060 standard; peptide: 24 AA.
AC ADF95060;
XX 26-FEB-2004 (first entry)
XX
XX Humanin peptide derivative D-Ser7/14 HN.
XX HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;
XX Alzheimer's disease.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 7
XX /note= "D-form residue"
XX
XX Misc-difference 14
XX /note= "D-form residue"
XX
XX WO2003097687-A2.
XX
XX 27-NOV-2003.
XX
XX 16-MAY-2003; 2003WO-JP006139.
XX
XX 16-MAY-2002; 2002US-0380958P.
XX
XX (NISH/) NISHIMOTO I.
XX
XX Nishimoto I;
XX
XX WPI; 2004-061983/06.
XX
XX New Humanin derivative that protects a neuronal cell from cytotoxicity,
XX useful for treating neurodegenerative disorders (e.g. Alzheimer's
XX disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated
XX amino acid.
XX
XX Claim 8; SEQ ID NO 9; 82pp; English.
XX
XX The invention relates to a derivative of humanin (HN) that protects a
XX neuronal cell from cytotoxicity, where the derivative contains at least
XX one D-amino acid or phosphorylated amino acid, or where the derivative
XX has an addition of one or more amino acids having an activity of forming
XX a multimer. The humanin derivatives are useful in protecting neuronal
XX cells from cytotoxicity related to neurodegenerative diseases. The
XX composition and method are useful in treating neurodegenerative
XX disorders, such as Alzheimer's disease. The present sequence represents a
XX HN peptide derivative.
XX
SQ Sequence 24 AA;
Query Match 100.0%; Score 120; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPRGFSCLLLTSEIDLVPVGRRA 24
1 MAPRGFSCLLLTSEIDLVPVGRRA 24
Db 1 MAPRGFSCLLLTSEIDLVPVGRRA 24

```

RESULT 11
ADP95052
ID ADP95052 standard; peptide; 24 AA.
XX
XX AC
XX ADP95052;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX DE Humanin (HN) wild-type peptide sequence.
XX
XX KW HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;
XX Alzheimer's disease.
XX
XX OS Homo sapiens.
XX
XX PN WO2003097687-A2.
XX
XX PD 27-NOV-2003.
XX
XX PE 16-MAY-2003; 2003WO-JP006139.
XX
XX PR 16-MAY-2002; 2002US-0380958P.
XX
XX PA (NISH/) NISHIMOTO I.
XX
XX PI Nishimoto I;
XX
XX DR WPI; 2004-061983/06.
XX
XX DR N-PSDB; ADP95077.
XX
XX PT New Humanin derivative that protects a neuronal cell from cytotoxicity,
XX useful for treating neurodegenerative disorders (e.g. Alzheimer's
XX disease); comprises a D-amino acid (e.g. D-serine) or a phosphorylated
XX amino acid.
XX
XX PS Example 1; SEQ ID NO 1; 82pp; English.
XX
XX
XX CC The invention relates to a derivative of humanin (HN) that protects a
XX CC neuronal cell from cytotoxicity, where the derivative contains at least
XX CC one D-amino acid or phosphorylated amino acid, or where the derivative
XX CC has an addition of one or more amino acids having an activity of forming
XX CC a multimer. The humanin derivatives are useful in protecting neuronal
XX CC cells from cytotoxicity related to neurodegenerative diseases. The
XX CC composition and method are useful in treating neurodegenerative
XX CC disorders, such as Alzheimer's disease. The present sequence represents a
XX CC HN wild-type peptide sequence.
XX
XX SQ Sequence 24 AA;
XX
XX
XX Query Match 100.0%; Score 120; DB 8; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-12;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MAPRGFSCLLLTSEIDLPIVKRA 24
XX |||||
XX DB 1 MAPRGFSCLLLTSEIDLPIVKRA 24
XX
XX
XX RESULT 12
XX ADP95057
XX ID ADP95057 standard; peptide; 24 AA.
XX
XX XX ADP95057;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX DE Humanin peptide derivative P-67/14 HN.
XX
XX KW HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;
XX Alzheimer's disease.
XX
XX OS Synthetic.
XX
XX OS Homo sapiens.

```

[illegible]

PF 16-MAY-2003; 2003WO-JP006139.
XX
XX 16-MAY-2002; 2002US-0380958P.
XX
XX (NISH/) NISHIMOTO I.
PA
XX Nishimoto I;
PI
XX WPI; 2004-061983/06.
DR
XX
XX New Humanin derivative that protects a neuronal cell from cytotoxicity,
PT useful for treating neurodegenerative disorders (e.g. Alzheimer's
PT disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated
PT amino acid.
XX
XX Example 1; SEQ ID NO 5; 82pp; English.
PS
XX The invention relates to a derivative of humanin (HN) that protects a
CC neuronal cell from cytotoxicity, where the derivative contains at least
CC one D-amino acid or phosphorylated amino acid, or where the derivative
CC has an addition of one or more amino acids having an activity of forming
CC a multimer. The humanin derivatives are useful in protecting neuronal
CC cells from cytotoxicity related to neurodegenerative diseases. The
CC composition and method are useful in treating neurodegenerative
CC disorders, such as Alzheimer's disease. The present sequence represents a
CC HN peptide derivative.
CC
XX
XX Sequence 24 AA;
SQ
Query Match 100.0%; Score 120; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MAPRGFSCLLLTSEIDLPIVRRRA 24
1 MAPRGFSCLLLTSEIDLPIVRRRA 24
DB
RESULT 14
ADP95078
ID ADF95078 standard; peptide; 24 AA.
XX
XX ADF95078;
AC
XX 26-FEB-2004 (first entry)
DT
XX
XX Humanin (HN) wild-type peptide sequence.
DE
XX HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;
KM Alzheimer's disease.
KM
XX Homo sapiens.
OS
XX WO2003097687-A2.
PN
XX
XX 27-NOV-2003.
PD
XX
XX 16-MAY-2003; 2003WO-JP006139.
PF
XX
XX 16-MAY-2002; 2002US-0380958P.
PR
XX
XX (NISH/) NISHIMOTO I.
PA
XX Nishimoto I;
PI
XX WPI; 2004-061983/06.
DR
XX N-PSDB; ADF95077.
XX
XX New Humanin derivative that protects a neuronal cell from cytotoxicity,
PT useful for treating neurodegenerative disorders (e.g. Alzheimer's
PT disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated
PT amino acid.
XX

PS Example; SEQ ID NO 27; 82pp; English.
XX
XX The invention relates to a derivative of humanin (HN) that protects a
CC neuronal cell from cytotoxicity, where the derivative contains at least
CC one D-amino acid or phosphorylated amino acid, or where the derivative
CC has an addition of one or more amino acids having an activity of forming
CC a multimer. The humanin derivatives are useful in protecting neuronal
CC cells from cytotoxicity related to neurodegenerative diseases. The
CC composition and method are useful in treating neurodegenerative
CC disorders, such as Alzheimer's disease. The present sequence represents a
CC HN wild-type peptide sequence.
CC
XX
XX Sequence 24 AA;
SQ
Query Match 100.0%; Score 120; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MAPRGFSCLLLTSEIDLPIVRRRA 24
1 MAPRGFSCLLLTSEIDLPIVRRRA 24
DB
RESULT 15
ADP95058
ID ADF95058 standard; peptide; 24 AA.
XX
XX ADF95058;
AC
XX 26-FEB-2004 (first entry)
DT
XX
XX Humanin peptide derivative D-Ser14 HN.
DE
XX HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;
KM Alzheimer's disease.
KM
XX Synthetic.
OS
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Misc-difference 14 /note="D-form residue"
FT
XX
XX WO2003097687-A2.
PN
XX
XX 27-NOV-2003.
PD
XX
XX 16-MAY-2003; 2003WO-JP006139.
PF
XX
XX 16-MAY-2002; 2002US-0380958P.
PR
XX
XX (NISH/) NISHIMOTO I.
PA
XX Nishimoto I;
PI
XX WPI; 2004-061983/06.
DR
XX
XX New Humanin derivative that protects a neuronal cell from cytotoxicity,
PT useful for treating neurodegenerative disorders (e.g. Alzheimer's
PT disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated
PT amino acid.
XX
XX Claim 8; SEQ ID NO 7; 82pp; English.
PS
XX The invention relates to a derivative of humanin (HN) that protects a
CC neuronal cell from cytotoxicity, where the derivative contains at least
CC one D-amino acid or phosphorylated amino acid, or where the derivative
CC has an addition of one or more amino acids having an activity of forming
CC a multimer. The humanin derivatives are useful in protecting neuronal
CC cells from cytotoxicity related to neurodegenerative diseases. The
CC composition and method are useful in treating neurodegenerative
CC disorders, such as Alzheimer's disease. The present sequence represents a
CC HN peptide derivative.
CC

XX Sequence 24 AA;

Query Match 100.0%; Score 120; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 1,3e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPRGFSCLLLTSEIDLPVKRRA 24
|||
Db 1 MAPRGFSCLLLTSEIDLPVKRRA 24

Search completed: March 28, 2006, 13:14:58
Job time : 18.78 secs

GenCore version 5.1.7
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* OM protein - protein search, using sw model

Run on: March 28, 2006, 13:15:18 ; Search time 3.136 Seconds
(without alignments)
736.353 Million cell updates/sec

Title: US-10-517-956-3
Perfect score: 120
Sequence: 1 MAPRGFSCLLLTSEIDLPIVKRRA 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	40.8	269	2	nitroreductase fam
2	46	38.3	359	2	transcription regu
3	45	37.5	220	2	hypothetical prote
4	44	36.7	90	2	prxs protein - Bnc
5	44	36.7	90	2	probable pheromone
6	44	36.7	92	1	hypothetical prote
7	44	36.7	107	2	hypothetical prote
8	44	36.7	610	2	hypothetical prote
9	44	36.7	1796	2	serine/threonine k
10	43.5	36.2	319	2	beta-galactosidase
11	43.5	36.2	1854	2	hypothetical prote
12	43	35.8	170	2	hypothetical prote
13	43	35.8	359	2	probable translati
14	43	35.8	540	2	probable phosphate
15	43	35.8	570	2	membrane associate
16	42	35.0	143	1	heat shock protein
17	42	35.0	207	2	hypothetical prote
18	42	35.0	262	1	indole-3-glycerol-
19	42	35.0	381	2	probable bacteriop
20	42	35.0	605	2	hypothetical prote
21	42	35.0	732	2	hypothetical prote
22	42	35.0	1584	2	protein P12M16.25
23	41.5	34.6	197	2	hypothetical prote
24	41	34.2	62	2	hypothetical prote
25	41	34.2	216	2	hypothetical prote
26	41	34.2	235	2	hypothetical prote
27	41	34.2	259	2	conserved hypotnet
28	41	34.2	264	2	hypothetical prote
29	41	34.2	378	2	probable malic enz

30	41	34.2	455	2	probable anthranil
31	41	34.2	543	2	tyrosine phosphata
32	41	34.2	582	2	hypothetical prote
33	41	34.2	612	2	protein P27015.4 l
34	41	34.2	732	2	hypothetical prote
35	41	34.2	1227	2	hypothetical prote
36	41	34.2	2052	2	phage-related prot
37	41	34.2	4196	2	dynein heavy chain
38	40.5	33.8	586	2	sensor histidine k
39	40.5	33.8	610	2	probable transport
40	40.5	33.8	610	2	probable transport
41	40.5	33.8	610	2	probable transport
42	40.5	33.8	723	2	hypothetical prote
43	40	33.3	159	2	hypothetical prote
44	40	33.3	159	2	hypothetical prote
45	40	33.3	176	2	conserved hypotnet

ALIGNMENTS

RESULT 1
F97327
nitroreductase family protein fused to ferredoxin domain [imported] - Clostridium acetob
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: F97327
R:Noiling, J.; Bennett, G.; Ometchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: F97327
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-269 <KIR>
A:Cross-references: UNIPROT:Q97D34; UNIPARC:UPI00000CA846; GB:AE001437; PIDD:AAK81409.1;
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3483

Query Match 40.8%; Score 49; DB 2; Length 269;
Best Local Similarity 50.0%; Pred. No. 3;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 RGFSCLLTSEIDLPI 19
DB 171 RGAPCLVLAIDVDLP 186

RESULT 2
AF3470
transcription regulator [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AF3470
R:DelVecchio, V.G.; Kapabert, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I
; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Lelesse
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi
A:Reference number: AD3252; PMID:11756688
A:Accession: AF3470
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <KOR>
A:Cross-references: UNIPROT:Q8YEX3; UNIPARC:UPI00000561B8; GB:AE008917; PIDD:AAJ52929.1;
C:Genetics:
A:Gene: BME11748
A:Map position: I

Query Match 38.3%; Score 46; DB 2; Length 359;
Best Local Similarity 43.5%; Pred. No. 12;

	Matches	10;	Conservative	3;	Mismatches	10;	Indels	0;	Gaps	0;
Qy	1	MAPRGSCLLITTSIDLPVKRR	23							
Db	116	MAVGSGCCVLLADNNGVPERR	138							

RESULT 3
H72717
hypothetical protein APE0282 - Aeropyrum pernix (strain K1)

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: H72717
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hakawa, Y.; Jin-no, K.; Takahashi, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawa, A.; Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic *Crenarchaeon*, *Aeropyrum*
#:Reference number: A72450; MUID:99310339; PMID:10382966

A/Accession: AF211
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-220 <KAN>
 A/Cross-references: UNIPROT:G9YEG0, UNIPARC:UPI000005DDA1, DDBJ:AP000059, NID:G5103911,
 A/Experimental source: strain K1
 C/Genetics:
 A/Gene: APB0282

Query Match	37.5%	Score 45	DB 2	Length 220
Best Local Similarity	47.6%	Pred. No. 11		
Matches 10; Conservative	4	Mismatches	7	Indels 0; Gaps 0;

```

QY      2 APRGSCLLLTSEIDLVPKR  22
          ||| ||| : ||| : |||
DB     194 APRPISLLTLPSPWSPVQR 214

```

RESULT 4

prgs protein Enterococcus faecalis plasmid pCF10
C/Species: Enterococcus faecalis
C/Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 07-May-1999
C/Accession: C56272
R/Chung, J.W.; Bensing, B.A.; Dunny, G.M.
J. Bacteriol. 177, 2107-2117, 1995
A/Title: Genetic analysis of a region of the Enterococcus faecalis plasmid pCF10 involved
in:Reference number: A56272; MUID:95236283; PMID:7721703

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 190 <FU>
A:Cross-references: UNIPARC:UPI000017AC31, GB:M64978
C:Genetics:
A:Gene: prgs
A:Genome: plasmid

Query Match	36.7%	Score 44	DB 2	length 90
Best Local Similarity	52.9%	Pred. No. 6.8		
Matches 9		Conservative 4	Mismatches 4	Indels 0
				Gaps 0

```

QY      8 CLLLTSEIDL PVKRA 24
          |||:|: :||: ||
Db     11 CLVLTNMRNLPIARLA 27

```

RESULT 5

E41662
 probable pheromone-responsive regulatory protein S - Enterococcus faecalis plasmid pCF10
 C:Species: Enterococcus faecalis
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1993
 C:Accession: E41662
 R:Kao, S.M.; Olmsted, S.B.; Vikenins, A.S.; Gallo, J.C.; Dunny, G.M.
 C:Biotechnol. 173, 7650-7664, 1991
 C:Biotechnol. 173, 7650-7664, 1991

A1Title: Molecular and genetic analysis of a region of plasmid pC10 containing positive tetracycline resistance.
A1Reference number: A41662; MUID:92041679; PMID:1938861

A:Reference number: A41662; NCID:92041679; PMID:19389651
A:Accession: E41662
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <K>
A:Cross-references: UNIPARC:UPI000017AC3; GB:M64978
C:Genetics:
A:Genome: plasmid

Query Match	36.7%	Score 44;	DB 2;	Length 90;
Best Local Similarity	52.9%	Pred. No. 6.8;		
Matches	9;	Conservative	4;	Mismatches 4; Indels 0; Gaps 0;

```
QY      8 CLLLTSEIDL PVKRA 24
      |||:|: :|: |
Db     11 CLVLTNMRNLPIARLA 27
```

RESULT 6

Hypothetical protein F-92 - *Escherichia coli*
 C:Species: *Escherichia coli*
 C:date: 05-Apr-1993 #sequence_revision 05-Apr-1993 #text_change 31-Dec-2004
 C:Accession: A04446
 R:Trso, J.Y.; Zalkin, H.; van Cleemput, M.; Yanofsky, C.; Smith, J.M.
 J. Biol. Chem. 257, 3525-3531, 1982
 A:Title: Nucleotide sequence of *Escherichia coli* purF and deduced amino acid sequence of
 A:Reference number: A92366; MUID:82142516; PMID:6277938

A:Accession: A04446
A:Molecule type: DNA
A:Residues: 1-92 <T50>
A:Cross-references: UNIPROT:P77203, UNIPARC:UPI0000174B06
C:Genetics:
A:Map position: 49 min

Query Match	36.7%	Score 44;	DB 1;	Length 92;
Best Local Similarity	58.8%	Pred. No. 6.9;		
Matches 10;	Conservative 1;	Mismatches 6;	Indels 0;	Gaps 0;

Qy 5 GFSCLLLTSEIDL Pvk 21
| | | | : | | |
Db 7 GISCDLQSSLFDPVK 23

RESULT 7

hypothetical protein TC0026 [imported] - Chlamydia muridarum (strain Nigg)
Cispecies: Chlamydia muridarum, Chlamydia trachomatis MoPn
CDate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
Accession: F81747
RReed, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A>Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
Reference number: AB1500; MUID:20150255; EMD:10684935

A:Accession: F22193
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <TET>
A:Cross-references: UNIPROT:Q9PLR9; UNIPARC:UPI0000055781; GB:AE002271; GB:AE002160; NID
A:Experimental source: strain N193 (MOPn)
C:Genetics:
A:Gene: TC0026
C:Superfamily: Chlamydia muridarum hypothetical protein TC0026

Query Match	36.7%	Score 44;	DB 2;	Length 107;
Best Local Similarity	47.4%	Pred. No. 8;		
Matches	9;	Conservative	1;	Mismatches 9;
				Indels 0;
				Gaps 0;

3 PRGSCLLLTSEIDL PVK 21
||| | | | :
QY

Db 86 PRGCCFWRLKREINCPFR 104

RESULT 8

576234

*hypothetical protein - *Synechocystis* sp. (strain PCC 6803)

C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: 576234

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.

A:Reference number: 574322; MUID:97061201; PMID:8905231

A:Accession: 576234

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-610 <KAW>

A:Cross-references: UNIPROT:P74396; UNIPARC:UPI00000C0E76; EMBL:D90914; GB:AB001339; NID A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match

Best Local Similarity 36.7%; Score 44; DB 2; Length 610;

Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 5 GPGSCLLLTSEIDLPVK 21

Db 18 GPGSCLEVLTLVMDGLK 34

RESULT 9

AC1895

serine/threonine kinase with two-component sensor domain alr0709 [imported] - *Neotoc* sp.

C:Species: *Neotoc* sp. PCC 7120

A:Note: *Neotoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AC1895

R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AC1895

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1796 <KUR>

A:Cross-references: UNIPROT:O8YYV3; UNIPARC:UPI00000CDE38; GB:BA000019; PIDN:BA072666.1;

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr0709

Query Match

Best Local Similarity 36.7%; Score 44; DB 2; Length 1796;

Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Oy 4 RGFGCLLTSEIDLPVK 21

Db 862 KALSCLENDLSEIDLPVK 879

RESULT 10

B42891

beta-galactosidase (EC 3.2.1.23), 36K chain - *Leuconostoc lactis* (strain NZ6009) plasmid

C:Species: *Leuconostoc lactis*

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C:Accession: B42891

R:David, S.; Stevens, H.; van Riel, M.; Simons, G.; de Vos, W.M.

J. Bacteriol. 174, 4475-4481, 1992

A:Title: *Leuconostoc lactis* beta-galactosidase is encoded by two overlapping genes.

A:Reference number: A42891; MUID:92325034; PMID:1624440

A:Accession: B42891

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-319 <DAV>

A:Cross-references: UNIPROT:Q02604; UNIPARC:UPI00001260F5; GB:M92281; NID:g149634; PIDN:

C:Keywords: glycosidase; hydrolase

Query Match

Best Local Similarity 36.2%; Score 43.5; DB 2; Length 319;

Matches 11; Conservative 4; Mismatches 7; Indels 7; Gaps 1;

Oy 2 APRGSCLLLTSEI-----DLPVKR 23

Db 249 APRFSCLPYPAELNATNTEIPLAR 277

RESULT 11

T13576

hypothetical protein 52C10.5 - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C:Accession: T13576

R:Benos, P.

submitted to the EMBL Data Library, February 1999

A:Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.

A:Reference number: 217690

A:Accession: T13576

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1854 <SEN>

A:Cross-references: UNIPROT:O96839; UNIPARC:UPI000008354E; EMBL:AL035311; NID:e1373062; I

C:Genetics:

A:Introns: 4/3; 53/3; 209/3; 962/1; 1632/1; 1666/2; 1739/1; 1793/1

A:Note: EG:52C10.5

Query Match

Best Local Similarity 36.2%; Score 43.5; DB 2; Length 1854;

Matches 12; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

Oy 3 PRGSCCLLTSEIDLPVKRRA 24

Db 714 PRGYCLLRGSNDELTVRVRVA 736

RESULT 12

H71063

hypothetical protein PH1206 - *Pyrococcus horikoshii*

C:Species: *Pyrococcus horikoshii*

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004

C:Accession: H71063

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatake, Y.; Hino, Y.; Yamamoto, S.; Sekine

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kuehida, N.; Oguchi,

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic ar

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: H71063

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-170 <KAW>

A:Cross-references: UNIPROT:O56978; UNIPARC:UPI0000063002; GB:AP000005; NID:g3236132; PIR

A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH1206

Query Match

Best Local Similarity 35.8%; Score 43; DB 2; Length 170;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 12 LTSEIDLPVKR 23

Db 103 LSSNIDIPVKR 114

RESULT 13
 B1566
 probable translation releasing factor RF-1 - Chlamydia trachomatis (serotype D, strain U
 C/Species: Chlamydia trachomatis
 C/Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 31-Dec-2004
 C/Accession: B71566
 R/Stephen, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
 Science 282, 754-759, 1998
 A/Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trach
 A/Reference number: A15170; MUID:99000809; PMID:9784135
 A/Accession: B71566
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-359 <ARN>
 A/Cross-references: UNIPROT:O84026; UNIPARC:UPI000013372A; GB:AE001277; GB:AE001273; NIT
 C/Genetics:
 A/Experimental source: serotype D, strain UW-3/Cx
 C/Superfamily: protein chain release factor, RF-1/RF-2
 A/Gene: pflA
 C/Query Match
 Best Local Similarity 35.8% Score 43; DB 2; Length 359;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 2 APRGSCLLLTSEIDL 18
 DB 139 ASKGQCEVLSTSESDL 155
 ||:|:|:|:|:|
 ||:|:|:|:|:|
 RESULT 14
 G83589
 probable phosphate transporter PA0450 [imported] - Pseudomonas aeruginosa (strain PA01)
 C/Species: Pseudomonas aeruginosa
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C/Accession: G83589
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; Lim,
 Nature 406, 959-964, 2000
 A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A/Reference number: A82950; MUID:20437337; PMID:10984043
 A/Accession: G83589
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-540 <STO>
 A/Cross-references: UNIPROT:O91668; UNIPARC:UPI00000C5060; GB:AE004482; GB:AE004091; NIT
 C/Genetics:
 A/Experimental source: strain PA01
 A/Gene: PA0450
 Qy Query Match 35.8% Score 43; DB 2; Length 540;
 Best Local Similarity 50.0% Pred. No. 57;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 Qy 5 GFSCLLLTSEIDLTPVKRA 24
 DB 220 GFACALLLALRLVKKRA 239
 ||:|:|:|:|:|
 ||:|:|:|:|:|
 RESULT 15
 H97244
 membrane associated methyl-accepting chemotaxis protein [imported] - Clostridium acetobu
 C/Species: Clostridium acetobutylicum
 C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C/Accession: H97244
 R/Nolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J. Bacteriol. 183, 4823-4838, 2001
 A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cid
 A/Reference number: A96900; MUID:21359325; PMID:21359325
 A/Accession: H97244
 A/Status: preliminary

```

A:Molecule type: DNA
A:Residues: 1-570 <KIR>
A:Cross-references: UNIPROT:Q97FD7; UNIPARC:UPI00000CA63B; GB:AE001437; PTDN:AAK80747.1;
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2803

Query Match          35.8%; Score 43; DB 2; Length 570;
Best Local Similarity 38.9%; Pred. No. 60;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY      4  RGFSCLLDLTSTSIDLPVK 21
      :|||:|:|:|:|:|
Db      350  KGFDCILQLONAVDKNIK 367

Search completed: March 28, 2006, 13:20:56
Job time : 4.136 secs

```

Search completed: March 28, 2006, 13:20:56
Job time : 4.136 secs

GenCore version 5.1.7
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*OM protein - protein search, using sw model

Run on: March 28, 2006, 13:10:33 ; Search time 19.008 Seconds
(without alignments)
890.819 Million cell updates/sec

Title: US-10-517-956-3
Perfect score: 120
Sequence: 1 MAPRGFSCLLLTSEIDLPIVKRRA 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	24	1 HUNIN HUMAN	Q81v9g homo sapien
2	49	40.8	269	2 Q87Dj4 CLOAB	Q87d14 clostridium
3	49	40.8	1181	2 Q55X85 CRYNE	Q55x85 cryptococcus
4	49	40.8	1181	2 Q5KMP8 CRYNE	Q5kmp8 cryptococcus
5	48	40.0	208	2 Q6FTB3 AZOCA	Q6ftb3 azotrizobiu
6	48	40.0	223	2 Q8FMY3 COREF	Q8fmy3 coriobacte
7	48	40.0	427	1 DPF3 CHICK	P58270 gallus gall
8	48	40.0	542	2 Q5R9C4 PONPY	Q5r9c4 pongo pygma
9	47.5	39.6	527	2 Q898A7 BRAJA	Q898a7 bradyrhizob
10	47	39.2	387	2 Q5BA28 EMENT	Q5ba28 aspergillus
11	47	39.2	532	2 Q4NML4 SMICC	Q4nml4 arthrobacte
12	47	39.2	2404	2 Q6LPT6 PLAF7	Q6lpt6 plasmodium
13	46	38.3	163	2 Q59U23 CANAL	Q59u23 candida alb
14	46	38.3	106	2 Q86126 BRAJA	Q86126 bradyrhizob
15	46	38.3	322	2 Q5TFH7 BRUAB	Q5tfh7 bruceella ab
16	46	38.3	359	2 Q8YEX3 BRUME	Q8yex3 bruceella me
17	46	38.3	399	2 Q424Y3 PLABE	Q424y3 plasmodium
18	46	38.3	551	2 Q98N27 RHILLO	Q98n27 rhizobium 1
19	46	38.3	1412	2 Q7RGZ8 PLAYO	Q7rgz8 plasmodium
20	45.5	37.9	412	2 Q9CU83 MOUSE	Q9cu83 mus musculu
21	45.5	37.9	490	1 FCXN33 HUMAN	FCXN33 homo sapien
22	45	37.5	50	2 Q64B16 SARCH	Q64b16 uncultured
23	45	37.5	106	2 Q59V29 CANAL	Q59v29 candida alb
24	45	37.5	111	2 Q82T01 PYRAB	Q82t01 pyrobaculum
25	45	37.5	220	2 Q9YFG0 ASRPP	Q9yfg0 aeropyrum p
26	45	37.5	322	2 Q5Y2B4 ARRYP	Q5y2b4 trypanosoma
27	45	37.5	326	2 Q54Q18 DICDI	Q54q18 dictyosteli
28	45	37.5	452	2 Q943G2 ORISA	Q943g2 oryza sativ
29	45	37.5	403	2 Q59UP4 CANAL	Q59up4 candida alb
30	45	37.5	652	2 Q7QPV8 GIALA	Q7qp8 glardia lam
31	45	37.5	783	2 Q7S0E8 NEUCR	Q7s0e8 neurospora

32	45	37.5	1110	2	Q4WDQ2 ASPRU	Q4wdq2 aspergillus
33	45	37.5	1273	2	Q4WR26 ASPRU	Q4wr26 aspergillus
34	45	37.5	1751	2	Q4WAX7 ASPRU	Q4wax7 aspergillus
35	45	37.5	1751	2	Q4WB48 ASPRU	Q4wb48 aspergillus
36	45	37.5	1761	2	Q4WB22 ASPRU	Q4wb22 aspergillus
37	45	37.5	2954	2	Q4IRV3 GIBZE	Q4irv3 gibberella
38	44.5	37.1	120	2	Q9PT93 BRARE	Q9pt93 brachydanio
39	44.5	37.1	263	2	Q5TYT5 BRARE	Q5tyt5 brachydanio
40	44.5	37.1	922	2	Q4WXJ9 ASPRU	Q4wxj9 aspergillus
41	44.5	37.1	1691	2	Q9GRP7 LEIMA	Q9grp7 leishmania
42	44	36.7	89	2	Q5BR02 SCHUA	Q5br02 schistosoma
43	44	36.7	98	2	Q5G3Q4 ENTFA	Q5g3q4 enterococcus
44	44	36.7	98	2	P77203 ECOLI	P77203 escherichia
45	44	36.7	107	2	Q9PLR9 CHLMU	Q9plr9 chlamydia m

ALIGNMENTS

RESULT 1

HUNIN HUMAN STANDARD; PRT; 24 AA.

AC Q81VGS:

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Humanin.

GN Name=HN;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.

RC TISSUE=Brain;

RX MEDLINE=21265469; PubMed=11371646; DOI=10.1073/pnas.101133498; Haahimoto Y., Ntikura T., Tajima H., Yasukawa T., Sudo H., Ito Y., Kita Y., Kawasumi M., Kouyama K., Doym M., Sobue G., Koide T., Tsuji S., Tang J., Aoihara K., Nishimoto I., "A rescue factor abolishing neuronal cell death by a wide spectrum of familial Alzheimer's disease genes and Abeta.", Proc. Natl. Acad. Sci. U.S.A. 98:6336-6341(2001).

RN [2]

RP NUCLEOTIDE SEQUENCE, AND INTERACTION WITH IGFBP3.

RX PubMed=14561895; DOI=10.1073/pnas.213511100; Ikonen M., Liu B., Haahimoto Y., Ma L., Lee K.W., Ntikura T., Nishimoto I., Cohen P., "Interaction between the Alzheimer's survival peptide humanin and insulin-like growth factor-binding protein 3 regulates cell survival and apoptosis.", Proc. Natl. Acad. Sci. U.S.A. 100:13042-13047(2003).

RN [3]

RP EVIDENCE OF IN VIVO EXPRESSION, AND TISSUE SPECIFICITY.

RC TISSUE=Brain;

RX MEDLINE=22007889; PubMed=12009529; DOI=10.1016/S0304-3940(02)00199-4; Tajima H., Ntikura T., Haahimoto Y., Ito Y., Kita Y., Terashita K., Yamazaki K., Koto A., Aiso S., Nishimoto I., "Evidence for in vivo production of Humanin peptide, a neuroprotective factor against Alzheimer's disease-related insults.", Neurosci. Lett. 324:227-231(2002).

RN [4]

RP FUNCTION, AND MUTAGENESIS OF 1-MET--ALA-2; 1-MET--PRO-3; CYS-8; SER-14; 19-PRO--ALA-24 AND 20-VAL--ALA-24.

RX PubMed=1171757;

RA Haahimoto Y., Ntikura T., Ito Y., Sudo H., Hata M., Arakawa E., Abe Y., Kita Y., Nishimoto I., "Detailed characterization of neuroprotection by a rescue factor humanin against various Alzheimer's disease-relevant insults.", J. Neurosci. 21:9235-9245(2001).

RN [5]

RP INTERACTION WITH BAX.

RX PubMed:12732850; DOI=10.1038/nature01627;
RA Guo B., Zhai D., Cabezas E., Welsh K., Nouraini S., Satterthwaite A.C.,
RA Reed J.C.;
RT "Humanin peptide suppresses apoptosis by interfering with Bax
RT activation.";
RL Nature 423:456-461(2003).
RN [6]
RP INTERACTION WITH TRIM11.
RX PubMed:12670303; DOI=10.1046/j.1460-9568.2003.02553.x;
RA Nishikawa T., Hashimoto Y., Tajima H., Ishizaka M., Yamagishi Y.,
RA Kawasumi M., Nawa M., Terashita K., Aiso S., Nishimoto I.;
RT "A tripartite motif protein TRIM11 binds and destabilizes Humanin, a
RT neuroprotective peptide against Alzheimer's disease-relevant
RT insults.";
RL Eur. J. Neurosci. 17:1150-1158(2003).
RN [7]
RP FUNCTION.
RX PubMed:15153530;
RA Ying G., Iribarren P., Zhou Y., Gong W., Zhang N., Yu Z.-X., Le Y.,
RA Cui Y., Wang J.M.;
RT "Humanin, a newly identified neuroprotective factor, uses the G
RT protein-coupled formylpeptide receptor-like-1 as a functional
RT receptor.";
RL J. Immunol. 172:7078-7085(2004).
CC -1- FUNCTION: Plays a role as a neuroprotective factor against death
CC induced by multiple different types of familial Alzheimer's
CC disease genes and beta amyloid in Alzheimer disease. Induced
CC chemotaxis of mononuclear phagocytes by using FPR1. Reduced the
CC aggregation and fibrillary formation by suppressing the effect of
CC APP on mononuclear phagocytes and acts by competitively inhibiting
CC the access of FPR1 to APP. Prevents the translocation of BAX from
CC cytosol to mitochondria.
CC -1- SUBUNIT: Interacts with IGFBR3, BAX and TRIM1.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed in the heart, skeletal muscles,
CC kidney and liver. Lesser but significant expression is observed in
CC the brain and the gastrointestinal tract. Expressed in the AD
CC brain, where it is found in some of the large intact neurons of
CC the occipital lobes and small and round reactive glial cells in
CC the hippocampus.
CC -1- INDUCTION: Release is regulated by intracellular mechanism. The
CC intracellular level is regulated by TRIM11 through the proteasomal
CC pathway.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AY029066; AAK50430.1; -; mRNA.
DR MM; 606120; -;
FT REGION 3 19 Responsible for the neuroprotective
FT activity.
FT COMPBIAS 9 12 Poly-Leu.
FT MUTAGEN 1 3 Missing: Abolishes the neuroprotective
FT activity.
FT MUTAGEN 1 2 Missing: No effect on the neuroprotective
FT activity.
FT MUTAGEN 8 8 C->A,D,E,F,G,I,L,M,N,P,Q,S,T,V,W,Y;
FT Abolishes the neuroprotective activity.
FT MUTAGEN 8 8 C->H: Significantly reduces the
FT neuroprotective activity.
FT MUTAGEN 8 8 C->K,R: No effect on the neuroprotective
FT activity.
FT MUTAGEN 14 14 S->A: Abolishes the neuroprotective
FT activity.
FT MUTAGEN 14 14 S->G: Potentiation of the neuroprotective
FT activity.
FT MUTAGEN 14 14 S->G: Potentiation of the neuroprotective
FT activity.
FT MUTAGEN 19 24 Missing: Abolishes the neuroprotective
FT activity.
FT MUTAGEN 20 24 Missing: No effect on the neuroprotective
FT activity.

SEQ SEQUENCE 24 AA; 2687 MW; 08B9A778EC13B971 CRC64;
Query Match 100.0%; Score 120; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4, 9e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPRGFSCILLTSEIDLPYKRA 24
DB 1 MAPRGFSCILLTSEIDLPYKRA 24
RESULT 2
ID Q97DU4_CLOAB PRELIMINARY; PRT; 269 AA.
AC Q97DU4;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Nitroreductase family protein fused to ferredoxin domain.
GN OrderedLocNames=CAC3483;
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OC NCBI_TaxID=1488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=1466286;
DOI=10.1128/JB.183.16.4823-4838.2001;
RA Noelling U., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe P., Doucette-Stamm L.A., Soucaille P.,
RA Daly M.U., Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AB007845; AAK81409.1; -; Genomic_DNA.
DR FTR; F97327; F97327.
DR HSP; P00193; 1DUR.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; F:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_Ferredoxin.
DR InterPro; IPR000415; Nitroreductase.
DR Pfam; PF00037; Fer4; 2.
DR Pfam; PF00881; Nitroreductase; 1.
DR PRINTS; PR00353; 4FE4SFDOXIN.
DR PROSITE; PS00198; 4FE4S_PRRRDOXIN; 2.
KW Complete proteome.
SQ SEQUENCE 269 AA; 30163 MW; BFE8734FBA3E951 CRC64;
Query Match 40.8%; Score 49; DB 2; Length 269;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 4 RGFSCLLTSEIDLP 19
DB 171 RGAPCLVATADYDFP 166
RESULT 3
ID Q55X85_CRYNE PRELIMINARY; PRT; 1181 AA.
AC Q55X85;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CNBBA4770;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.

```

OX NCBI_TaxID=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
  Wicker B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
  preliminary data.
DR EMBL; AB01000011; EAL22302.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1181 AA; 130133 MW; 825BF00F2CDD4C00 CRC64;

Query March 40.8%; Score 49; DB 2; Length 1181;
Best Local Similarity 41.7%; Pred. No. 1.1e+02;
Matches 10; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MAPRGSCLLLTSEIDLPIVKRR 24
Db 379 LRPRALTCLLLSODTFDPVPRHDA 402

RESULT 4
OSKMP8 CRYNE
ID OSKMP8 CRYNE PRELIMINARY; PRT; 1181 AA.
AC OSKMP8;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CNB00940;
OS Cryptococcus neoformans var. neoformans JEC21.
OC Bakaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=214684;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JEC21;
RA Loftus B., Amedeo P., Roncaglia P., Vamathavan J., Uteback T.,
  Van Aken S., Fraser C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JEC21;
RA Donlin M.;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=JEC21;
RX PubMed=15653466; DOI=10.1126/science.1103773;
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
  Vamathavan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
  Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
  D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
  Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywnicki M.I.,
  Kwon-Chung K.J., Lengele K.B., Malet R., Marra M.A., Marra R.E.,
  Mathewson C.A., Mitchell T.G., Perlea W., Riggs F.R., Salzberg S.L.,
  Schlein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
  Suh B.B., Tenney A., Uteback T.R., Wicker B.L., Mortman J.R.,
  Wye N.H., Kronstad J.W., Lodge J.K., Heltman J., Davis R.W.,
  Fraser C.M., Hyman R.W.;
RT "The genome of the basidiomycetous yeast and human pathogen
  Cryptococcus neoformans.";
RL Science 307:1321-1324 (2005).
DR EMBL; AB017342; AA041793.1; -; Genomic_DNA.
DR InterPro; IPR011989; ARM-1like.
DR InterPro; IPR000357; HEAT.
DR Pfam; PF02985; HEAT; 2.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1181 AA; 130134 MW; 825BF00F2CDD4C00 CRC64;

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Query March 40.8%; Score 49; DB 2; Length 1181;
Best Local Similarity 41.7%; Pred. No. 1.1e+02;
Matches 10; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MAPRGSCLLLTSEIDLPIVKRR 24
Db 379 LRPRALTCLLLSODTFDPVPRHDA 402

RESULT 5
OSKMP8 AZOCA
ID OSKMP8 AZOCA PRELIMINARY; PRT; 208 AA.
AC OSKMP8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE hupD.
GN Name=hupD;
OS Azorhizobium caulinodans.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hypnomicrobacteriaceae; Azorhizobium.
OX NCBI_TaxID=7;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ORS571;
RX MEDLINE=2235395; PubMed=12324339;
RX DOI=10.1128/AEM.68.10.4915-4924.2002;
RA Baginsky C., Brito B., Imperial J., Palacios J.M., Ruiz-Argueso T.;
RT "Diversity and evolution of hydrogenase systems in rhizobia.";
RL Appl. Environ. Microbiol. 68:4915-4924 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ORS571;
RX PubMed=15321689; DOI=10.1016/j.fems.2004.07.003;
RA Baginsky C., Palacios J.M., Imperial J., Ruiz-Argueso T., Brito B.;
RT "Molecular and functional characterization of the Azorhizobium
  caulinodans ORS571 hydrogenase gene cluster.";
RL FEMS Microbiol. Lett. 237:399-405 (2004).
RN EMBL; AY581127; AAS91029.1; -; Genomic_DNA.
DR GO; GO:0009375; C:ferredoxin hydrogenase complex; IEA.
DR GO; GO:0008801; F:ferredoxin hydrogenase activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0016485; P:protein processing; IEA.
DR InterPro; IPR006671; Peptidase M52.
DR InterPro; IPR004419; Pept_M52_HyD.
DR InterPro; IPR006227; Pept_M52_mat.
DR Pfam; PF01750; Hycl; 1.
DR PRINTS; PR00446; HYDRGNUPRAK.
DR TIGRFAMs; TIGR00140; hupD.fthd.pepf.1.
DR TIGRFAMs; TIGR00141; hupD.fthd.pepf.1.
DR TIGRFAMs; TIGR00072; hupD.fthd.pepf.1.
SQ SEQUENCE 208 AA; 22061 MW; 75CCTB4B280B3724 CRC64;

Query March 40.8%; Score 48; DB 2; Length 208;
Best Local Similarity 47.8%; Pred. No. 27;
Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MAPRGSCLLLTSEIDLPIVKRR 23
Db 142 VAPAVVEVLTLTSEIDLPVPR 164

RESULT 6
OSKMP9 COREP
ID OSKMP9 COREP PRELIMINARY; PRT; 223 AA.
AC OSKMP9;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Putative carboxylase.
GN OrderedLocNames=CE2360;
OS Corynebacterium efficiens.

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OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC SRRAIN-VS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RX MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Ueda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeno K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens."
RL Genome Res. 13:1572-1579(2003).
DR EMBL; BA000035; BAC19170.1; -; Genomic DNA.
DR GO; GO:0009320; C:phosphoribosylaminoimidazole carboxylase co. .; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR GO; GO:0004638; F:phosphoribosylaminoimidazole carboxylase ac. .; IEA.
DR GO; GO:0006189; P:de novo IMP biosynthesis; IEA.
DR InterPro; IPR000031; AIR_carboxyl.
DR ProDom; PD002193; AIR_carboxyl; 1.
KM Complete proteome.
SQ SEQUENCE 223 AA; 22873 MW; EAAAS4A0152C54D1 CRC64;

Query Match 40.0%; Score 48; DB 2; Length 223;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 PRGSCLLLTSTEDLPVKRA 24
DB 91 PRGSLVLTAGTSDFPAREA 112

RESULT 7
DP33_CHICK STANDARD; PRT; 427 AA.
AC PS8270;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Zinc-finger protein DP33 (cer-d4).
GN Name=DP33; Synonyms=CERD4;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3 AND 4).
RX MEDLINE=21833813; PubMed=11845289; DOI=10.1007/s00335-001-3039-1;
RA Ninkina N.N., Merilov I.B., Kulikova D.A., Allinova-Kost M.V.,
RA Simonova O.B., Korochkin L.I., Kiselev S.L., Buchman V.L.;
RT "Cerd4, third member of the d4 gene family; expression and
RT organization of genomic locus."
RL Mamm. Genome 12:862-866(2001).
CC -1- FUNCTION: Probably involved in RNA transcription.
CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=P58270-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P58270-2; Sequence=VSP_005614, VSP_005615;
CC Name=3;
CC IsoId=P58270-3; Sequence=VSP_005614, VSP_005616;
CC Name=4;
CC IsoId=P58270-4; Sequence=VSP_005614, VSP_005615, VSP_005616;
CC -1- SIMILARITY: Belongs to the regulon/DPF family.
CC -1- SIMILARITY: Contains 1 C2H2-type zinc finger.
CC -1- SIMILARITY: Contains 2 PHD-type zinc fingers.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF362754; AAK51968.1; -; mRNA.
DR EMBL; AF362753; AAK51967.1; -; mRNA.
DR EMBL; AF362756; AAK51970.1; -; mRNA.
DR EMBL; AF362755; AAK51969.1; -; mRNA.
DR HSSP; Q14839; 1M2.
DR Ensemble; ENSGALG0000009352; Gallus gallus.
DR InterPro; IPR000637; AT hook DNA_bd.
DR InterPro; IPR007087; ZnF_C2H2.
DR InterPro; IPR001965; ZnF_PHD.
DR InterPro; IPR001841; ZnF_RING.
DR Pfam; PF00628; PHD; 2.
DR Pfam; PF00096; zf-C2H2; 1.
DR PRINTS; PR00929; ATHOOK.
DR SMART; SM00249; PHD; 2.
DR SMART; SM00184; RING; 2.
DR SMART; SM00355; ZnF_C2H2; 1.
DR PROSITE; PS01359; ZF_PHD_1; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
KW Alternative splicing; Metal-binding; Nuclear protein; Repeat;
KT Transcription; Transcription regulation; Zinc; Zinc-finger.
FT ZN_FING 247 270
FT ZN_FING 308 368
FT ZN_FING 365 415
FT ZN_FING 102 137
FT VARSPPLIC 102 137
FT Missing {in isoform 2, isoform 3 and
FT /FTId=VSP_005614.
FT VARSPPLIC 212 224
FT Missing {in isoform 2 and isoform 4}.
FT /FTId=VSP_005615.
FT VARSPPLIC 340 427
FT LKDDCDRGYHNYCINPVPEPESGMSCHLRELLREAS
FT AFGQA -> AHIGRRGRDEAPRTTDLRGSTSESST
FT TFHGFDDDAEPLSRGGGCGGSSPSADKKGC (1n
FT isoform 3 and isoform 4).
FT /FTId=VSP_005616.
SQ SEQUENCE 427 AA; 48930 MW; B22DB85D1E714152 CRC64;

Query Match 40.0%; Score 48; DB 1; Length 427;
Best Local Similarity 52.6%; Pred. No. 56;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 RGRSCLLLTSTEDLPVKR 22
DB 126 RRPSCKLYTSEVDLPKK 144

RESULT 8
QSR9C4_PONPY PRELIMINARY; PRT; 542 AA.
AC QSR9C4;
DT 01-FEB-2005 (T-EMBLrel. 29, Created)
DT 01-FEB-2005 (T-EMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (T-EMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp469B1012.
GN Name=DKFZp469B1012;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP TISSUE=Kidney;
RC The German cDNA Consortium;
RA Wamburt R., Heubner D., Mewes H.W., Well B., Amld C., Osanger A.,
RA Fodor G., Han M., Wiemann S.;

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RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR859465; CAH91636.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0015075; F:ion transporter activity; IEA.
 DR GO; GO:0015293; F:symporter activity; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR GO; GO:0006814; P:sodium ion transport; IEA.
 DR InterPro; IPR007114; MIPS.
 DR InterPro; IPR011701; MIPS.1.
 DR InterPro; IPR004749; Orycat_transp.
 DR InterPro; IPR005829; Sug_transporter.
 DR Pfam; PF07690; MIPS_1; 1.
 DR TIGRFAMs; TIGR00896; 2A0119; 1.
 DR PROSITE; PS00850; MIPS; 1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 542 AA; 59847 MW; PAF2EI4949E711B0 CRC64;

Query Match 40.0%; Score 48; DB 2; Length 542;
 Best Local Similarity 64.3%; Pred. No. 71;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 PRGSCULLLT---SEIDLPVKRRA 24
 Db 423 PSFSCFLFLYTSSEL 436

RESULT 9
 Q89887_BRAJA PRELIMINARY; PRT; 527 AA.
 ID Q89887_BRAJA PRELIMINARY; PRT; 527 AA.
 AC Q89887;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE B117200 protein.
 GN OrderedLocusNames=B117200;
 OS Bradyrhizobium japonicum.
 OC Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OC NCBI_TaxID=375;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=USDA 110;
 RX MEDLINB=22484998; PubMed=12597275;
 RA Kaneo T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Idegawa K., Iritschi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110.";
 RT DNA Res. 9:189-197(2002).
 RL EMBL; BA000040; BAC52465.1; -; Genomic DNA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000914; SBP_bac_5.
 DR InterPro; IPR005311; Tst.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00496; SBP_bac_5; 1.
 DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
 KM Complete proteome.
 SQ SEQUENCE 527 AA; 57740 MW; 7ECBE31BFB1C0FCS CRC64;

Query Match 39.6%; Score 47.5; DB 2; Length 527;
 Best Local Similarity 44.0%; Pred. No. 84;
 Matches 11; Conservative 3; Mismatches 8; Indels 3; Gaps 1;

QY 3 PRGSCULLLT---SEIDLPVKRRA 24
 Db 281 PRGYACMLRLNHLQPPFDPNPAVRRA 305

RESULT 10
 Q5BA28_EMENI PRELIMINARY; PRT; 387 AA.
 ID Q5BA28_EMENI PRELIMINARY; PRT; 387 AA.
 AC Q5BA28;
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=AN2602.2;
 OS Aspergillus nidulans FGSC A4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eukaryota; Trichocomaceae; Smeritella.
 OC NCBI_TaxID=227321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FGSC A4;
 RA Birren B., Nussbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Archchil H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Chepel Y., Collymore A., Cook A., Cooke P., Corum B., Deatellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
 RA Gardyna S., Genette S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrum J., Menes L.,
 RA Minova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Puthkang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schupbach R., Seaman S., Severy C., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Testaye S., Theodore J., Tophan K., Travers M.,
 RA Vaasiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander B.;
 RT "Genome Sequence of Aspergillus nidulans."
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AAC0100043; EAA64707.1; -; Genomic DNA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR000379; Ser esters.
 DR Hydrolase; Hypothetical protein.
 SQ SEQUENCE 387 AA; 42761 MW; ACCJ314337251054 CRC64;

Query Match 39.2%; Score 47; DB 2; Length 387;
 Best Local Similarity 75.0%; Pred. No. 74;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 13 TSEIDLPVKRRA 24
 Db 60 TSEIQIPLKRRRA 71

RESULT 11
 Q4ANML4_9M1CC PRELIMINARY; PRT; 532 AA.
 ID Q4ANML4_9M1CC PRELIMINARY; PRT; 532 AA.
 AC Q4ANML4;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Similar to Sugar diacid utilization regulator.
 GN ORFNames=ArthDRAPT_3900;
 OS Arthrobacter sp. FB24.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococciaceae; Micrococccaceae; Arthrobacter.
 OC NCBI_TaxID=290399;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FB24;
 RG US DOE Joint Genome Institute (JGI-PGP);

RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israeli S., Pitluck S., Richardson P.,
RT "Sequencing of the draft genome assembly of *Archaeobacter* sp. FB24.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (PGF-ORNL);
RA Laximier F., Land M.;
RT "Annotation of the draft genome assembly of *Archaeobacter* sp. FB24.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAGG01000001; EAL98032.1; -; Genomic DNA.
SQ SEQUENCE 532 AA; 57662 MW; 58148F8B1D07465F CRC64;

Query Match 39.2%; Score 47; DB 2; Length 532;
Best Local Similarity 45.0%; Pred. No. 1e+02; Mismatches 0; Gaps 0;
Matches 9; Conservative 4; Indels 0;

Cy 3 PRGFCLLLTSEIDL PVK 22
Db 14 PLGFASLILRSPRSDPIER 33

RESULT 12
06LF76_PLAF7 PRELIMINARY; PRT; 2404 AA.
ID 06LF76_PLAF7
AC 06LF76;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Protein kinase, putative).
GN ORFNames=PF1145C;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=3D7;
RX MEDLINE=2255708; PubMed=1236867; DOI=10.1038/nature01095;
RA Hall N., Pain A., Berriman M., Churchev C., Harris B., Harris D.,
RA Hingl K., Bowman S., Atkin R., Baker S., Barton A., Brooks K.,
RA Buckee C.O., Burrows C., Chervach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Cotton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauber H., Hornby T., Holroyd S., Horrocks F.,
RA Humphrey S., Jagels K., James K.D., Johnson D., Kethornou A.,
RA Knights A., Konfortov B., Kyes K., Larke N., Lawson D., Leonard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabbittowitch R.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Thayer A., Unwin L., Whitehead S., Woodward J.,
RA Salsdon J.E., Craig A., Newbold C., Barrell B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=3D7;
RA Chervach I., Davis P., Goodhead I., Stevens K., Mungall K.,
RA Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
RA Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.G.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382400; CAG25050.1; -; Genomic DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000715; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.

DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00659; Kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
KM Hypothetical protein, Kinase.
SQ SEQUENCE 2404 AA; 279784 MW; E0162E3ABD024B4 CRC64;

Query Match 39.2%; Score 47; DB 2; Length 2404;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Cy 1 MAPRGSCLLLTSEIDL 18
Db 2308 MAPETSCCTEYETEKIDI 2325

RESULT 13
Q59U23_CANAL PRELIMINARY; PRT; 106 AA.
ID Q59U23_CANAL
AC Q59U23;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Ca019.3748;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitospore Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federapfel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tsung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the genome of *Candida albicans*.";
RT Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACQ01000127; EAK94320.1; -; Genomic DNA.
KM Hypothetical protein.
SQ SEQUENCE 106 AA; 11772 MW; 33DF49BDC1305C8 CRC64;

Query Match 38.3%; Score 46; DB 2; Length 106;
Best Local Similarity 61.5%; Pred. No. 30;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Cy 9 LLLTSEIDL PVK 21
Db 70 LLLTTEIDQPIK 82

RESULT 14
086126_BRAJA PRELIMINARY; PRT; 163 AA.
ID 086126_BRAJA
AC 086126; Q79V08;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Bl0903 protein).
GN OrderedLocNames=Blr0903;

Search completed: March 28, 2006, 13:20:02
Job time : 21.008 secs

OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=110BPC4;
RX MEDLINE=98348447; PubMed=9683482;
RA Bauer E., Kaspar T., Fischer H.M., Hennecke H.;
RT "Expression of fixK_{hfa} operon in Bradyrhizobium japonicum depends on
a new response regulator system, RegR.";
*RT J. Bacteriol. 180:3853-3863(1998).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=USDA 110;
RC MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Matsumoto M., Shimpo S., Tsunoda H., Wada T., Yamada M.,
RA Kohara M., Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AJ006100; CAA06860.1; -; Genomic_DNA.
DR EMBL; BA000040; BAC46168.1; -; Genomic_DNA.
DR InterPro; IPR009394; DUF1052.
DR Pfam; PF06319; DUF1052; 1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 163 AA; 18262 MW; 192132E03DE83D6 CRC64;

Query Match 38.3%; Score 46; DB 2; Length 163;
Best Local Similarity 55.0%; Pred. No. 45;
Matches 11; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 5 GFSCLLTSEIDLPIYKRR 24
DB 37 GFSCI---SELPLPSGRR 52

RESULT 15
Q57FH7 BRUB
ID Q57FH7_BRUB PRELIMINARY; PRT; 322 AA.
AC Q57FH7;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Transcriptional regulator, P_{is} family.
GN OrderedLocustNames=Brubi_0196;
OS Brucella abortus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=235;
RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=9-941 / Biovar 1;
RX PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;
RA Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuermer R.L.,
RA Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.;
RT "Completion of the genome sequence of Brucella abortus and comparison
to the highly similar genomes of Brucella melitensis and Brucella
suis.";
*RT J. Bacteriol. 187:2715-2726(2005).
RL EMBL; AE017223; AAX73607.1; -; Genomic_DNA.
KM Complete proteome.
SQ SEQUENCE 322 AA; 34746 MW; 2C912CFPE235402A CRC64;

Query Match 38.3%; Score 46; DB 2; Length 322;
Best Local Similarity 43.5%; Pred. No. 90;
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MAPRGFSCLLTSEIDLPIYKRR 23
DB 79 MAVGVGCVTLADNNGVPIYRR 101

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OM protein - protein search, using SW model

Run on: March 28, 2006, 13:20:18 / Search time 4.288 Seconds
(without alignments)
462.737 Million cell updates/sec

Title: US-10-517-956-3
Perfect score: 120
Sequence: 1 MAPRGFSCLLLTSEIDLVPVKRRA 24

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/PCrus_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	40.0	466	2	US-09-902-540-11091, A Sequence 11091, A
2	45	37.5	460	2	US-09-248-796A-16093, A Sequence 16093, A
3	43	35.8	145	2	US-09-252-991A-18594, A Sequence 18594, A
4	43	35.8	178	2	US-09-252-991A-17622, A Sequence 17622, A
5	43	35.8	537	1	US-08-647-397-2, A Sequence 2, Appl1
6	43	35.8	597	2	US-09-252-991A-22560, A Sequence 22560, A
7	42	35.0	109	1	US-08-647-397-4, A Sequence 4, Appl1
8	42	35.0	138	2	US-09-489-039A-11748, A Sequence 11748, A
9	42	35.0	542	2	US-09-614-891-10, A Sequence 10, Appl1
10	41.5	34.6	338	2	US-09-902-540-15112, A Sequence 15112, A
11	41	34.2	113	2	US-09-489-039A-12316, A Sequence 12316, A
12	41	34.2	155	2	US-09-489-039A-9041, A Sequence 9041, A
13	41	34.2	228	2	US-09-182-145-19, A Sequence 19, Appl1
14	41	34.2	229	2	US-09-182-145-99, A Sequence 99, Appl1
15	41	34.2	230	2	US-09-182-145-98, A Sequence 98, Appl1
16	41	34.2	231	2	US-09-182-145-97, A Sequence 97, Appl1
17	41	34.2	232	2	US-09-182-145-96, A Sequence 96, Appl1
18	41	34.2	233	2	US-09-182-145-95, A Sequence 95, Appl1
19	41	34.2	234	2	US-09-182-145-94, A Sequence 94, Appl1
20	41	34.2	235	2	US-09-182-145-93, A Sequence 93, Appl1
21	41	34.2	236	2	US-09-182-145-92, A Sequence 92, Appl1
22	41	34.2	237	2	US-09-182-145-91, A Sequence 91, Appl1
23	41	34.2	238	2	US-09-182-145-90, A Sequence 90, Appl1
24	41	34.2	239	2	US-09-182-145-89, A Sequence 89, Appl1
25	41	34.2	240	2	US-09-182-145-88, A Sequence 88, Appl1
26	41	34.2	241	2	US-09-182-145-87, A Sequence 87, Appl1
27	41	34.2	242	2	US-09-182-145-86, A Sequence 86, Appl1

28	41	34.2	243	2	US-09-182-145-85, A Sequence 85, Appl1
29	41	34.2	244	2	US-09-182-145-84, A Sequence 84, Appl1
30	41	34.2	245	2	US-09-182-145-83, A Sequence 83, Appl1
31	41	34.2	246	2	US-09-182-145-82, A Sequence 82, Appl1
32	41	34.2	247	2	US-09-182-145-81, A Sequence 81, Appl1
33	41	34.2	248	2	US-09-182-145-80, A Sequence 80, Appl1
34	41	34.2	249	2	US-09-182-145-79, A Sequence 79, Appl1
35	41	34.2	250	2	US-09-182-145-78, A Sequence 78, Appl1
36	41	34.2	251	2	US-09-182-145-77, A Sequence 77, Appl1
37	41	34.2	252	2	US-09-252-991A-19237, A Sequence 19237, A
38	41	34.2	253	2	US-09-252-991A-31986, A Sequence 31986, A
39	41	34.2	254	2	US-09-457-0468-72, A Sequence 72, Appl1
40	41	34.2	255	2	US-09-866-5708-72, A Sequence 72, Appl1
41	41	34.2	256	2	US-09-252-991A-20739, A Sequence 20739, A
42	41	34.2	257	2	US-09-987-691A-4, A Sequence 4, Appl1
43	41	34.2	258	2	US-09-987-691A-2, A Sequence 2, Appl1
44	40.5	33.8	259	2	US-09-182-145-87, A Sequence 87, Appl1
45	40	33.3	260	1	US-07-966-187-4, A Sequence 4, Appl1

ALIGNMENTS

```
RESULT 1
US-09-902-540-11091
Sequence 11091, A Application US/0902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11091
LENGTH: 466
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-11091

Query Match 40.0%; Score 48; DB 2; Length 466;
Best Local Similarity 48.3%; Pred. No. 6.8;
Matches 14; Conservative 2; Mismatches 7; Indels 6; Gaps 1;

Oy 2 APRGFSCLLTSEIDLVPVKRRA 24
Db 411 APRGFSARGFGLLVPEODLVVYMA 439

RESULT 2
US-09-248-796A-16093
Sequence 16093, A Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Welnslock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 16093
LENGTH: 460
TYPE: PRT
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; ORGANISM: Candida albicans
US-09-248-796A-16093
Query Match 37.5%; Score 45; DB 2; Length 460;
Best Local Similarity 47.4%; Pred. No. 22;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MAPRGFSCLLLTSEIDLP 19
Db 159 IAPRGNSCPICLTDDFPV 177

RESULT 3
US-09-252-991A-18594
; Sequence 18594, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18594
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18594

Query Match 35.8%; Score 43; DB 2; Length 145;
Best Local Similarity 47.4%; Pred. No. 13;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 APRGFSCLLTSEIDLPV 20
Db 29 APRMACCCVMTAIIIRPM 47

RESULT 4
US-09-252-991A-17622
; Sequence 17622, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17622
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17622

Query Match 35.8%; Score 43; DB 2; Length 178;
Best Local Similarity 57.1%; Pred. No. 16;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LLTSEIDLPVKRR 23
Db 88 LVLRERLDLPVRR 101
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```

RESULT 5
US-08-647-397-2
; Sequence 2, Application US/08647397
; Patent No. 5972702
; GENERAL INFORMATION:
; APPLICANT: Belter, David R.
; APPLICANT: Brady, Kevin P.
; TITLE OF INVENTION: OSTEOCLAST TRANSPORTER
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacke, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,397
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: B0801/7048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 537 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-647-397-2

Query Match 35.8%; Score 43; DB 1; Length 537;
Best Local Similarity 55.6%; Pred. No. 60;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 6 FSCLLLTSEIDLPVKRR 23
Db 426 FSCFLYTSFLYPTVLARQ 443

RESULT 6
US-09-252-991A-22560
; Sequence 22560, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22560
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22560

Query Match 35.8%; Score 43; DB 2; Length 597;
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Best Local Similarity 50.0%; Pred. No. 67;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
Qy 5 FSCLLLTSEIDPVKRR 24
Db 277 GFACALLLALLRLVKKRA 296

RESULT 7

US-08-647-397-4
Sequence 4, Application US/08647397
Patent No. 5972702
GENERAL INFORMATION:
APPLICANT: Beier, David R.
APPLICANT: Brady, Kevin P.
TITLE OF INVENTION: OSTEOCLAST TRANSPORTER
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,397
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0801/7048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-647-397-4

Query Match 35.0%; Score 42; DB 1; Length 109;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 6 FSCLLLTSEI 16
Db 57 FSCFLPTYSL 67

RESULT 8
US-09-489-039A-11748
Sequence 11748, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLABSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11748
LENGTH: 138
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11748

Query Match 35.0%; Score 42; DB 2; Length 138;
Best Local Similarity 46.7%; Pred. No. 18;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 9 LLLTSEIDPVKRR 23
Db 43 VIEVTSNVEYVKKR 57

RESULT 9

US-09-614-891-10
Sequence 10, Application US/09614891
Patent No. 6680379
GENERAL INFORMATION:
APPLICANT: SUN, WILLIAM
TITLE OF INVENTION: ORGANIC ANION TRANSPORTER GENES AND PROTEINS
FILE REFERENCE: 030727.0022.CIP.1
CURRENT APPLICATION NUMBER: US/09/614,891
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,771
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 542
TYPE: PRT
ORGANISM: Homo sapiens
US-09-614-891-10

Query Match 35.0%; Score 42; DB 2; Length 542;
Best Local Similarity 72.7%; Pred. No. 90;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FSCLLLTSEI 16
Db 426 FSCFLPTYSL 436

RESULT 10
US-09-902-540-15112
Sequence 15112, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 15112
LENGTH: 338
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-15112

Query Match 34.6%; Score 41.5; DB 2; Length 338;
Best Local Similarity 40.0%; Pred. No. 63;
Matches 8; Conservative 6; Mismatches 5; Indels 1; Gaps 1;


```
RESULT 15
US-09-182-145-98
; Sequence 98, Application US/09182145B
; Patent NO. 6387657
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/09/182,145B
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: US 60/063,704
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: US 60/073,612
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: US 60/081,695
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 98
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-182-145-98

Query March 34.2%; Score 41; DB 2; Length 230;
Best Local Similarity 46.7%; Pred. No. 48;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 5 GFSCILLITSEIDLP 19
||:||||:|:|
Db 106 GFTCLPLCSEDPRLP 120
```

Search completed: March 28, 2006, 13:22:08
Job time : 4.288 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:15:18 ; Search time 45.864 Seconds
(Without alignments)
736.353 Million cell updates/sec

Title: US-10-517-956-1

Perfect score: 1817

Sequence: 1 METNFSPTNXYEBSVYESA.....TNDTANSSAPPAETLQAM 351

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:0:0
2: p1r2:0:0
3: p1r3:0:0
4: p1r4:0:0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1817	100.0	351	2	B42009 FMLP-related recep
2	1318	72.5	353	2	B42009 FMLP-related recep
3	1249.5	68.8	350	2	A42009 N-formyl peptide r
4	1223.5	67.3	352	2	A46520 N-formyl peptide r
5	1174.5	64.6	364	2	A49542 N-formyl peptide c
6	538.5	29.6	371	2	JC5498 G protein-coupled
7	530.5	29.2	473	2	JC5835 anaphylatoxin C3a
8	513	28.2	350	1	A37963 complement C5a ana
9	509.5	28.0	482	2	S65766 G protein-coupled
10	502	27.7	371	2	JC5796 Probable chemotatr
11	500	27.6	353	2	JC2492 G protein-coupled
12	500	27.5	352	1	S27357 complement C5a ana
13	499	27.5	355	2	A55733 G protein-coupled
14	457.5	25.2	351	1	A46525 complement C5a ana
15	430.5	23.7	359	2	JC2134 angiotensin II rec
16	426.5	23.5	359	2	JH0611 angiotensin II rec
17	426.5	23.5	359	2	JC1104 angiotensin II rec
18	426.5	23.5	360	2	A5611 angiotensin-8 rece
19	423.5	23.3	359	2	S15433 angiotensin II rec
20	422.5	23.3	355	2	JQ1231 interleukin-8 rece
21	420.5	23.1	359	2	JQ1516 angiotensin II rec
22	420.5	23.1	359	2	A42656 angiotensin II rec
23	419.5	23.1	352	2	A45747 neuropeptide Y/pep
24	418.5	23.0	359	2	I39418 angiotensin II rec
25	418.5	23.0	359	2	A48425 angiotensin II rec
26	418	22.8	359	2	A44425 angiotensin II rec
27	413.5	22.8	352	2	G00048 fusin (LRSTR) - C
28	413.5	22.8	359	2	JC1194 angiotensin II rec
29	412	22.7	362	2	A30341 G protein-coupled

30	411.5	22.6	353	2	S28787 neuropeptide Y/pep
31	411.5	22.6	362	2	U0694 angiotensin II rec
32	405.5	22.3	359	2	I51372 angiotensin II rec
33	405	22.3	418	2	A46226 somatostatin recep
34	403	22.2	359	2	A48921 interleukin-8 rece
35	402	22.1	398	2	I56517 mu opioid receptor
36	402	22.1	428	2	S30508 probable G protein
37	401	22.1	356	2	S42096 interleukin-8 rece
38	401	22.1	358	2	A53752 interleukin-8 rece
39	401	22.1	398	2	A57510 mu opioid receptor
40	399.5	22.0	350	2	A39445 interleukin-8 rece
41	399.5	22.0	391	2	A41795 somatostatin recep
42	399.5	22.0	391	2	C41795 somatostatin recep
43	399.5	22.0	391	2	A39297 mu opioid receptor
44	397	21.8	398	2	I56504 mu opioid receptor
45	396	21.8	392	2	S65693 opioid receptor mu

ALIGNMENTS

RESULT 1
B42009
FMLP-related receptor 1 - human
N/Alternate names: FMLP receptor homolog FPR2; formyl peptide receptor like-1; Probable C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence revision 14-Jul-1995 #text change 09-Jul-2004
C/Accession: B42009; JCI258; JQ1521; A42492; I54751; S21581
R/Bao, L.; Gerard, N.P.; Rddy Jr., R.L.; Shows, T.B.; Gerard, C.
Genomics 13, 437-440, 1992
A/Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR), A/Reference number: A42009; MUID:92307681; PMID:1612600
A/Accession: B42009
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-263, 'A', 265-338, 'C', 340-351 <BAO>
A/Cross-references: UNIPROT:P25090; UNIPARC:UPI0000177808; GB:M76672
A/Note: Authors translated the codons GTG for residue 15 as Glu, TCT for residue 19 as Tr
R/Perez, H.D.; Holmes, R.; Kelly, E.; McClary, J.; Andrews, W.H.
Gene 118, 303-304, 1992
A/Title: Cloning of a cDNA encoding a receptor related to the formyl peptide receptor of A/Reference number: JCI258; MUID:92380523; PMID:1511907
A/Accession: JCI258
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-351 <PER>
A/Cross-references: UNIPARC:UPI00000012D0; EMBL:X63819; NID:g31460; PID:g31461
A/Experimental source: bone marrow mRNA
R/Re, R.D.; Cavanagh, S.L.; Quehenberger, O.; Prossnitz, E.R.; Cochran, C.G.
Biochem. Biophys. Res. Commun. 184, 582-589, 1992
A/Title: Isolation of a cDNA that encodes a novel granulocyte N-formyl peptide receptor. A/Reference number: JQ1521; MUID:92246937; PMID:1374236
A/Accession: JQ1521
A/Molecule type: mRNA
A/Residues: 1-351 <YE2>
A/Cross-references: UNIPARC:UPI00000012D0; GB:M88107; NID:g189862; PID:g189863
A/Experimental source: granulocytes
A/Note: formyl peptide-stimulated calcium mobilization comparable to that of the formyl I R/Murphy, P.M.; Ozcelik, T.; Kenney, R.T.; Tiffany, H.L.; McDermott, D.; Francke, U.
J. Biol. Chem. 267, 7637-7643, 1992
A/Title: A structural homologue of the N-formyl peptide receptor. Characterization and c A/Reference number: A42492; MUID:92218423; PMID:1373134
A/Accession: A42492
A/Molecule type: mRNA
A/Residues: 1-351 <MUR>
A/Cross-references: UNIPARC:UPI00000012D0; GB:M84562; NID:g182741; PINN:AAA52473.1; PID:g A/Note: sequence extracted from NCBI backbone (NCBIN:94159, NCBIIP:94160)
R/Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A/Title: Molecular cloning of cDNAs encoding a IJ78 receptor and putative leukocyte chem A/Reference number: I54751; MUID:94092629; PMID:7505609
A/Accession: I54751
A/Status: preliminary; translated from GB/EMBL/DBJ

A,Molecule type: mRNA
A:Residues: 1-351 <RES>
A:Cross-references: UNIPARC:UPI000000120D; GB:D10922; NID:g219864; PIDN:BA01720.1; PID:
C:Comment: This G-protein coupled receptor, homologue to the N-formyl peptide receptor
differentiated myeloid cells and is probably a chemotactic receptor for some other ligand
C:Genetics:
A:Gene: GDB:PPRL1
A:Cross-references: GDB:127554; OMIM:136538
A:Map position: 19q13.3-19q13.4
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keyordfamily: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein
F/27-53/Domain: transmembrane #status predicted <TM1>
F/59-83/Domain: transmembrane #status predicted <TM2>
F/100-121/Domain: transmembrane #status predicted <TM3>
F/145-169/Domain: transmembrane #status predicted <TM4>
F/206-226/Domain: transmembrane #status predicted <TM5>
F/242-266/Domain: transmembrane #status predicted <TM6>
F/282-307/Domain: transmembrane #status predicted <TM7>
F/4/Binding site: carbohydrate (Aen) (covalent) #status predicted
F/98-176/Dissulfide bonds: #status predicted

Query Match 100.0%; Score 1817; DB 2; Length 351;
Best Local Similarity 100.0%; Pred. NO.5.4e-145;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEXBEVSAGYTVLRILPLVVLGTVFVLGVLGVLVWAGFRMTRTYT 60
Db 1 METNFTPLNEXBEVSAGYTVLRILPLVVLGTVFVLGVLGVLVWAGFRMTRTYT 60
QY 61 TTCYLMALADSFATLPLPLIVSMANGKMPGWLCKLIHIVVDINLFGSVLIGFLA 120
Db 61 TTCYLMALADSFATLPLPLIVSMANGKMPGWLCKLIHIVVDINLFGSVLIGFLA 120
QY 121 LDRICIVLHPVNAQNRTVSLAMKVIVGPIALVLTLPVFLFTVTPINGDTCTFNF 180
Db 121 LDRICIVLHPVNAQNRTVSLAMKVIVGPIALVLTLPVFLFTVTPINGDTCTFNF 180
QY 181 ASWGTPEERLKVATIMLTARGIIRFVIGSLPMSIVALCYGLIAKIHKKMKISSRPL 240
Db 181 ASWGTPEERLKVATIMLTARGIIRFVIGSLPMSIVALCYGLIAKIHKKMKISSRPL 240
QY 241 RVTAVVASFFICWPPQVALIGTWLKMELFYGKKIIDIIVNPSSLAFFNSCLNPM 300
Db 241 RVTAVVASFFICWPPQVALIGTWLKMELFYGKKIIDIIVNPSSLAFFNSCLNPM 300
QY 301 LVYFVGQDPRERLHSLPSTLSEALSSEDAPTNDTANASPPAETELQAM 351
Db 301 LVYFVGQDPRERLHSLPSTLSEALSSEDAPTNDTANASPPAETELQAM 351

RESULT 2

* C42009
FMLP-related receptor 2 - human
N:Alternate names: FMLP-related receptor I; probable chemotactic receptor FPRH2
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: C42009
R:Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.
Genomics 13, 437-440, 1992
A:Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR),
A:Reference number: A42009; MUID:92307681; PMID:1612600
A:Accession: C42009
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-353 <BAO>
A:Cross-references: UNIPROT:P25089; UNIPARC:UPI0000050485; GB:M76673; NID:g182668; PID:g
C:Comment: This Fmet-Leu-Phe receptor homolog, whose ligand is not yet known, appears to
C:Genetics:
A:Gene: GDB:PPRL2
A:Cross-references: GDB:112885; OMIM:136539
A:Map position: 19q13.3-19q13.4
A:Introns: #status absent

C:Superfamily: vertebrate rhodopsin
C:Keyordfamily: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein
Query Match 72.5%; Score 1318; DB 2; Length 353;
Best Local Similarity 71.7%; Pred. No. 4e-103;
Matches 253; Conservative 39; Mismatches 59; Indels 2; Gaps 1;

QY 1 METNFTPLNEXBEVSAGYTVLRILPLVVLGTVFVLGVLGVLVWAGFRMTRTYT 60
Db 1 METNFTPLNEXBEVSAGYTVLRILPLVVLGTVFVLGVLGVLVWAGFRMTRTYT 60
QY 61 TTCYLMALADSFATLPLPLIVSMANGKMPGWLCKLIHIVVDINLFGSVLIGFLA 120
Db 61 TTCYLMALADSFATLPLPLIVSMANGKMPGWLCKLIHIVVDINLFGSVLIGFLA 120
QY 121 LDRICIVLHPVNAQNRTVSLAMKVIVGPIALVLTLPVFLFTVTPINGDTCTFNF 180
Db 121 LDRICIVLHPVNAQNRTVSLAMKVIVGPIALVLTLPVFLFTVTPINGDTCTFNF 180
QY 181 ASWGTPEERLKVATIMLTARGIIRFVIGSLPMSIVALCYGLIAKIHKKMKISSRPL 240
Db 181 ASWGTPEERLKVATIMLTARGIIRFVIGSLPMSIVALCYGLIAKIHKKMKISSRPL 240
QY 241 RVTAVVASFFICWPPQVALIGTWLKMELFYGKKIIDIIVNPSSLAFFNSCLNPM 300
Db 241 RVTAVVASFFICWPPQVALIGTWLKMELFYGKKIIDIIVNPSSLAFFNSCLNPM 300
QY 301 LVYFVGQDPRERLHSLPSTLSEALSSEDAPTNDTANASPPAETELQAM 351
Db 301 LVYFVGQDPRERLHSLPSTLSEALSSEDAPTNDTANASPPAETELQAM 351

RESULT 3

A42009
N-formyl peptide receptor - human
N:Alternate names: FMLP receptor
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
C:Accession: JC2014; A36309; A35495; A42009; I52414
R:Murphy, P.M.; Tiffany, H.L.; McDermott, D.; Ahuja, S.K.
Gene 133, 285-290, 1993
A:Title: Sequence and organization of the human N-formyl peptide receptor-encoding gene.
A:Reference number: JC2014; MUID:94040825; PMID:8224916
A:Accession: JC2014
A:Molecule type: mRNA
A:Residues: 1-350 <MUR>
A:Cross-references: UNIPROT:P21462; UNIPARC:UPI000016A92F; GB:L10820; NID:g182739; PIDN:1
A:Reference number: A36309; MUID:91105045; PMID:2176894
A:Accession: A36309
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-191, 'N', 193-345, 'E', 347-350 <BOU1>
A:Note: The sequence in Genbank entry HUNNPPR, release 112.0, (PIDN:AAA36362.1) has the
R:Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.
Genomics 13, 437-440, 1992
A:Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR),
A:Reference number: A42009; MUID:92307681; PMID:1612600
A:Accession: A42009
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA

A;Residues: 1,'G',3-28,30-100,'L',102-104,106-112,'FLA',115-176,178-182,184-191,'N',194
 A;Cross-references: UNIPARC:UPI00001778DA
 R;Perez, H.D.; Holmes, R.; Kelly, E.; McClary, J.; Chou, Q.; Andrews, W.H.
 Biochemistry 31, 11595-11599, 1992
 A;Title: Cloning of the gene coding for a human receptor for formyl peptides. Characteri
 A;Reference number: 152414; MUID:53075765; PMID:1445895
 A;Accession: 152414
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-5 <PER>
 A;Cross-references: UNIPARC:UPI000011EA63; GB:649810; NID:g260832; PIDN:AAD14906.1; PID:
 C;Genetic8: GDB:PPRI
 A;Gene: GDB:PPRI
 A;Cross-references: GDB:127999; OMIM:136537
 A;Map position: 19q13.4-19q13.4
 A;Intons: #status absent
 A;Note: entire coding region is found in exon 3; alternatively spliced mRNA transcripts
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein
 F;27-53/Domain: transmembrane #status predicted <TM1>
 F;59-83/Domain: transmembrane #status predicted <TM2>
 F;100-121/Domain: transmembrane #status predicted <TM3>
 F;145-169/Domain: transmembrane #status predicted <TM4>
 F;206-225/Domain: transmembrane #status predicted <TM5>
 F;242-266/Domain: transmembrane #status predicted <TM6>
 F;279-304/Domain: transmembrane #status predicted <TM7>
 F;4,10/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;98-176/Distufide bonds: #status predicted

Query Match 68.8%; Score 1249.5; DB 2; Length 350;
 Best Local Similarity 68.9%; Pred. No. 2-2e-97;
 Matches 241; Conservative 37; Mismatches 71; Indels 1; Gaps 1;

QY 1 METNFSPLNBYEVSAGYTVLRILPLVVLGTVLGNGLVYVAGPFRMTVT 60
 DB 1 METNSSLPNTISGTPVAVSAGYLFLLITVLPVAVTVLGLGGLVYVAGPFRMTVT 60
 QY 61 TICLYNLALADFSFTATLPPLIVSWAMGEKMPFGMLCKLHIIVDINLFGSVFLIGFIA 120
 DB 61 TICLYNLALADFSFTATLPPLIVSWAMGEKMPFGMLCKLHIIVDINLFGSVFLIGFIA 120
 QY 121 LDRICVLAHPVMAQNHRVSLAMKVIYVGPWIALVLTLPVFLFTTTPYTGKTCFNF 180
 DB 121 LDRICVLAHPVMAQNHRVSLAMKVIYVGPWIALVLTLPVFLFTTTPYTGKTCFNF 180
 QY 121 LDRICVLAHPVMAQNHRVSLAMKVIYVGPWIALVLTLPVFLFTTTPYTGKTCFNF 180
 DB 121 LDRICVLAHPVMAQNHRVSLAMKVIYVGPWIALVLTLPVFLFTTTPYTGKTCFNF 180
 QY 181 ASWCGTPEERLKVATIMLTARGIIRFVIGSLPMSIYACGLIAAKIHKMKTKSRPL 240
 DB 181 SPWTDNPKERIKVAVVAVLTVRGIIRFVIGSLPMSIYAVSGLIATKIHQGLTKSRPL 240
 QY 241 RVLTAVVASPFIQWPFQVALLGLTWLKEMLFGKTKIIDILVNPSSLAFFNSCLNPM 300
 DB 241 RVLSFVAAAFPLCSPQVALLGLTWLKEMLFGKTKIIDILVNPSSLAFFNSCLNPM 299
 QY 301 LVYVVGQDFRRLIHSPLTSERLSEDSAPNTDANSAAPPATELQAM 350
 DB 300 LVYVVGQDFRRLIHSPLTSERLSEDSAPNTDANSAAPPATELQAM 349

RESULT 4 -

A46520
 N-formyl peptide receptor - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A46520
 R;Ye, R.D.; Quehenberger, O.; Thomas, K.M.; Navarro, J.; Cavanagh, S.L.; Prosenitz, E.R.
 J. Immunol. 150, 1383-1394, 1993
 A;Title: The rabbit neutrophil N-formyl peptide receptor. cDNA cloning, expression, and
 A;Reference number: A46520; MUID:53163563; PMID:8432984
 A;Accession: A46520
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-352 <YE1>
 A;Cross-references: UNIPROT:Q05394; UNIPARC:UPI000012AA43; GB:M94549; NID:g165027; PIDN:

A;Experimental source: NZM, neutrophils
 A;Note: sequence extracted from NCBI backbone (NCBI:P124908)
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 67.3%; Score 1223.5; DB 2; Length 352;
 Best Local Similarity 67.7%; Pred. No. 3.4e-95;
 Matches 239; Conservative 41; Mismatches 70; Indels 3; Gaps 2;

QY 1 METNFSPLNBYEVSAGYTVLRILPLVVLGTVLGNGLVYVAGPFRMTVT 60
 DB 1 MDNNSLPNVSGTQATPRLVGLVDFVSLILVTVFVGLGNGLVYVAGPFRMTVT 60
 QY 61 TICLYNLALADFSFTATLPPLIVSWAMGEKMPFGMLCKLHIIVDINLFGSVFLIGFIA 120
 DB 61 TICLYNLALADFSFTATLPPLIVSWAMGEKMPFGMLCKLHIIVDINLFGSVFLIGFIA 120
 QY 121 LDRICVLAHPVMAQNHRVSLAMKVIYVGPWIALVLTLPVFLFTTTPYTGKTCFNF 178
 DB 121 LDRICVLAHPVMAQNHRVSLAMKVIYVGPWIALVLTLPVFLFTTTPYTGKTCFNF 180
 QY 179 NFASWGTPEERLKVATIMLTARGIIRFVIGSLPMSIYACGLIAAKIHKMKTKSR 238
 DB 181 DWSPTEDPKERIKVATIMLTARGIIRFVIGSLPMSIYACGLIAAKIHKMKTKSR 240
 QY 239 PLVLTAVVASPFIQWPFQVALLGLTWLKEMLFGKTKIIDILVNPSSLAFFNSCLN 298
 DB 241 PLVLTAVVASPFIQWPFQVALLGLTWLKEMLFGKTKIIDILVNPSSLAFFNSCLN 299
 QY 299 PMLYVVGQDFRRLIHSPLTSERLSEDSAPNTDANSAAPPATELQAM 351
 DB 300 PMLYVVGQDFRRLIHSPLTSERLSEDSAPNTDANSAAPPATELQAM 352

RESULT 5

A49542
 N-formyl peptide chemotactic receptor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C;Accession: A49542
 R;Geo, J.L.; Murphy, P.M.
 J. Biol. Chem. 268, 25395-25401, 1993
 A;Title: Species and subtype variants of the N-formyl peptide chemotactic receptor reveal
 A;Reference number: A49542; MUID:94064602; PMID:8244972
 A;Accession: A49542
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-364 <GHO>
 A;Cross-references: UNIPROT:P33766; UNIPARC:UPI00000210BF; GB:L22181; NID:g347396; PIDN:
 C;Genetic8:
 A;Intons: #status absent
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: chemotaxis; transmembrane protein

Query Match 64.6%; Score 1174.5; DB 2; Length 364;
 Best Local Similarity 64.6%; Pred. No. 4.6e-91;
 Matches 237; Conservative 38; Mismatches 73; Indels 19; Gaps 5;

QY 1 METNFSPLNBYEVSAGYTVLRILPLVVLGTVLGNGLVYVAGPFRMTVT 52
 DB 1 MDNNSLPNVSGTQATPRLVGLVDFVSLILVTVFVGLGNGLVYVAGPFRMTVT 60
 QY 53 FRMTATVTTTCYNTALADFSFTATLPPLIVSWAMGEKMPFGMLCKLHIIVDINLFGS 112
 DB 61 FRMTATVTTTCYNTALADFSFTATLPPLIVSWAMGEKMPFGMLCKLHIIVDINLFGS 120
 QY 113 VFLIGTALDRICVLAHPVMAQNHRVSLAMKVIYVGPWIALVLTLPVFLFTTTPYTGKTCFNF 171
 DB 121 VFLIGTALDRICVLAHPVMAQNHRVSLAMKVIYVGPWIALVLTLPVFLFTTTPYTGKTCFNF 178
 QY 172 ----GDTTCFNFASWGTPEERLKVATIMLTARGIIRFVIGSLPMSIYACGLIAAK 227
 DB 179 RLPDGTACTFDFSPWTKDPEERKVAVTMLTVRGIIRFVIGSLPMSIYACGLIAAK 238

Query 228 HHKMMKISSRRLATRLTVVVASFFICMPFQOLVALGTVMLKEMFYKRYKIIDLVNPT 287
Db 229 IHRQGLISSLRRLKRLVSLFVNAFFLCWCPQVVALISTIQVERLKNMTPGLVVAL-KIT 297
Qy 288 SSIAPFNSCLNPMVLVVFVQODFRERLIHSLPSTLERALSSEDSAPTNDYPAAN---SASPAA 344
Db 298 SPLAPFNSCLNPMVLVVFVQODFRERLIHSLPSTLERALSSEDSAPTNDYPAAN---SASPAA 357
Qy 345 ETELQAM 351
Db 358 ENTLNAM 364

RESULT 6
JC5498
G protein-coupled receptor DEZ - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C:Accession: JCS498
R:Meinhart, A.; Herney, G.; Schinke, B.; Hermanns-Borgmeyer, I.
Biochem. Biophys. Res. Commun. 233, 336-342, 1997
A:Title: A novel G protein-coupled receptor with homology to neuropeptide and chemotactic peptide
A:Reference number: JC5498; MUID:97289630; PMID:9144535
A:Contents: Brain
A:Accession: JCS498
A:Molecule type: mRNA
A:Residues: 1-371 <MET>
A:Cross-References: UNIPROT:P97468; UNIPARC:UPI00000269A9; GB:U79525; NID:91732346; PIDD
C:Comment: This protein is involved in the bone metabolism.
C:Superfamily: vertebrate rhodopsin
F:110-187/Dissulfide bonds: #status predicted

Query Match 29 6%; Score 538.5; DB 2; Length 371;
Best Local Similarity 35.2%; Pred. No. 1,1e-37;
Matches 120; Conservative 70; Mismatches 124; Indels 27; Gaps 8;

Qy 10 NEVER-----VSYSAGYTVLRILP---LVVLGVTFTVGLNGGLVIVWAGFRMTRVTVT 61
Db 14 DEISGPGFYFDLEASWEAKVAPVFLVIVLSVCFGLGNGLVIVIAIFKKKRYNT 73
Qy 62 IGYNLALADFSFTATLPFLIVSMAGKWPFGWFLCKLHVVDINLFGSVFLGPIAL 121
Db 74 VMPVLAADLEFLNFIPLMHITVYAMDYHWYFGKMKCKISNPLSHMYTSVPLLVISF 133
Qy 122 DRICIVLHPWAQNRRTSLAMKVIYGPWIIALVLTLPVFLFTVTPNDYCTNFA 181
Db 134 DRCISVLTPVWSQNRISRLIYMTCSAVVLAFLISSSLVFRDPAI--HGKITCFNPPS 192
Qy 182 SMGGTPEERLKYATIMTLARG-----IRFVIGFSLPMSIYACGLIAAKIHKKGM 233
Db 193 L--AAPESHPPASQVSVTGSRRVAVTVTRFLCGFLIPFIIITACLTIVFLQGNRL 250
Qy 234 IKSSRPLRLVTAIVVASFICMPFQOLVALGTVMLKEMFYGKKYKIIDLVNP--TSSLAF 292
Db 251 AKKKKPFKIIITIIITFPLCWCPYH-----TLYLBLEHTAVDSVSFSLGLPLATAVAI 304
Qy 293 FNSCLNPMVLVVFVQODFRERLIHSLPSTLERALSSEDSAPTNDYPAAN---SASPAA 344
Db 305 ANSCNPMPLVVFVQODFRERLIHSLPSTLERALSSEDSAPTNDYPAAN---SASPAA 357

RESULT 7
JC5835
anaphylatoxin C3a receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: JC5835
R:Fukunaka, Y.; Ember, J.A.; Hugli, T.E.
Biochem. Biophys. Res. Commun. 242, 663-668, 1998
A:Title: Cloning and characterization of rat C3a receptor: Differential expression of rat
A:Reference number: JC5835; MUID:98125550; PMID:9464274
A:Accession: JC5835

A:Molecule type: mRNA
A:Residues: 1-473 <FUK>
A:Cross-references: UNIPROT:O55197; UNIPARC:UPI0000126C12; GB:U86379; NID:g3015534; PIDN:
A:Experimental source: brain
C:Comment: This receptor plays a role in the central nervous systems.
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein
F:322-51/Domain: transmembrane #status predicted <TM1>
F:58-83/Domain: transmembrane #status predicted <TM2>
F:96-118/Domain: transmembrane #status predicted <TM3>
F:138-160/Domain: transmembrane #status predicted <TM4>
F:322-347/Domain: transmembrane #status predicted <TM5>
F:367-392/Domain: transmembrane #status predicted <TM6>
F:406-433/Domain: transmembrane #status predicted <TM7>
F:9,201/Binding site: carboxylate (Asn) (covalent) #status predicted
F:360/Binding site: phosphate (Ser) (covalent) [by protein kinase C] #status predicted

Query Match 29.2% Score 530.5; DB 2; Length 473;
Best Local Similarity 28.9%; Pred. No. 6, 5e-37;
Matches 133; Conservative 60; Mismatches 107; Indels 161; Gaps 10;

DY 27 ILPLVLGVTVFLGYLGNGLVITWAGFRMTVTYTCYLNLADSFPTLRPLIVSMA 86
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 24 IASVILSLTCLGLPQNGLVLMVAGVKRKRTNTVTFLLTLADFLCCLSLFSVAHLI 83
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DY 87 MGKRPFGMFLCKLIHIVDINLPQSVEFLGPIALDRICCVLHPWAQNRRYSLSMKVI 146
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 84 LRGHNPYGLFLCKLPSVILIIMFPASVFLLTALSIDRCIMVHKPIQONHRSVTAFAVC 143
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DY 147 VGPATIALVLTLPVLEFLTITVTTPNGDTY--CTFNPA----- 182
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 144 GCWVVTVTVMCIPEVTRDLVY---DDYSGCYNPDSSRAYDWDMYNSHLPEINPPD 200
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DY 183 -----N----- 183
DB 201 NSTGVVDRTAPSSSVPARDLWTATTALOSQTHTSPEDPFSGDSASQQPHYGAKPTVL 260
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DY 184 ----GTPEERLK----- 192
DB 261 IATPGGFVEDHKNKTINTGAFLSAHTESPSTASSPYAHDPDDYPDQLMYGNHAWT 320
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DY 193 --VAITMLTAGRIIFPVIGFSLPMISIVACYGIIAKHKKGMIRK-SRRLRYLTVAVAS 249
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 321 POVALT-----ISLVGEFLVPFTMITCTSYLVERMKNTLTRSRNKTLRAVAAVTV 374
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DY 250 FFICWFEPQLVALLGTTW----LKEMLFYGGKYKIIDIVNPPTSIAFFNSCLNPMLYVF 304
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 375 FVFCMIPRHVIGILVITTDGSALREVLPMDMSI-----ALASANSCTNPFIYAL 426
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DY 305 VGQDFRERLIHSLPTSLRALSED SAPINDTANASAPPAE 345
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 427 LKDFPKRKAROSVKGLEAFSEEL--THSTCTODKAPSK 465
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 8
A37963
Complement Csa anaphylatoxin receptor - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence revision 14-Feb-1997 #extc_change 09-Jul-2004
C:Accession: A37963; S13646; T52417; S30518
R:Boulay, F.; Wery, L.; Tardif, M.; Brouillon, L.; Vignais, P.
Biochemistry 30, 2993-2999, 1991
A>Title: Expression cloning of a receptor for Csa anaphylatoxin on differentiated HL-60 c
A:Reference number: A37963; MUID:91175748; PMID:2007135
A:Accession: A37963
A:Molecule type: mRNA
A:Residues: 1-350 <BOU>
A:Cross-references: UNIPROT:P21730; UNIPARC:UPI0000000C99; GB:J05327; NID:G179699; PIDN:
R:Gerard, N.P.; Gerard, C.
Nature 349, 614-617, 1991
A>Title: The chemotactic receptor for human Csa anaphylatoxin.
A:Reference number: S13646; MUID:91156029; PMID:1847994
A:Accession: S13646

A: Molecule type: mRNA
A: Residues: 1-350 <GER>
A: Cross-references: UNIPARC:UPI000000C99; EMBL:X56674; NID:929568; PIDN:CA837830.1; PIR:Biocchem. N.P.; Bao, L.; Xiao-Ping, H.; Eddy, R.L.
Biochemistry 32, 1243-1250, 1993
A: Title: Human chemotaxis receptor genes cluster at 19q13.3-13.4. Characterization of the
A: Reference number: 152417; MUID:93192225; PMID:8383526
A: Accession: 152417
A: Status: translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-3 <RES>
A: Cross-references: UNIPARC:UPI000011B869; GB:S56556; GB:S56557; NID:g298577; NID:g29857
C: Genes: GDB:CSRI; CSA; CSAR
A: Gene: GDB:CSRI; CSA; CSAR
A: Cross-references: GDB:128856; OMIM:113995
A: Map position: 19q13.3-19q13.4
A: Introns: 1/3
A: Note: the list of introns may be incomplete
C: Function:
A: Description: mediates the inflammatory and chemotactic responses of polymorphonuclear
n
C: Superfamily: vertebrate rhodopsin
C: Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymor
P: 1-37/Domain: extracellular #status predicted <EX1>
P: 38-61/Domain: transmembrane #status predicted <TM1>
P: 62-71/Domain: intracellular #status predicted <IM1>
P: 72-94/Domain: transmembrane #status predicted <TM2>
P: 95-110/Domain: extracellular #status predicted <EX2>
P: 111-132/Domain: transmembrane #status predicted <TM3>
P: 133-149/Domain: intracellular #status predicted <IM2>
P: 150-174/Domain: transmembrane #status predicted <TM4>
P: 175-206/Domain: extracellular #status predicted <EX3>
P: 207-227/Domain: transmembrane #status predicted <TM5>
P: 228-242/Domain: intracellular #status predicted <IM3>
P: 243-264/Domain: transmembrane #status predicted <TM6>
P: 265-283/Domain: extracellular #status predicted <EX4>
P: 284-307/Domain: transmembrane #status predicted <TM7>
P: 308-350/Domain: intracellular #status predicted <IM4>
P: 5/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 28.2%; Score 513; DB 1; Length 350;
Best Local Similarity 33.6%; Pred. No. 1,4e-35;
Matches 122; Conservative 60; Mismatches 129; Indels 52; Gaps 9;

QY 4 NPSTP-LNEYEB-----VSYSAGYTVLRILPLVVGTVFVLGNGLVIVVAGF 53
DB 5 NYTPDYGHAYDDKOTLDLNPVDKTSNTLAKVPDILALIVAVVFLVGNALVWVTA 64
QY 54 RMTRTVTTCYLMALADFSFTATLPPLIVSMAMGKMPGFWLCKLHIVVDINLFGSV 113
DB 65 EAKRTIVAMFNLAVADPISCLALPLFTSIQHHMHPFGAACSILPSLILNMYASI 124
QY 114 PLIGFIALDRCICYLHNVAMQNHRTVSLANKVIVGPITLALVLTLPFLPLTTVTI 173
DB 125 LLLATISADPFLVFKPIWQNFAGLAWIACAVAGLALLLTPISFLRVV-----RE 179
QY 174 TY-----CTFNPSWGTPEBRRLKVAITMLTARGIIRFVIGSPISVIAICGLIA 227
DB 180 EYPPPKVLCAVDYSH-----DKRRERAV-----AIVRLVAGFIMPLLTITICTF 228
QY 228 IHKKMISRSRPLRLTAVVASPFICMPFQVALLAGTWMKELFYGKYKIIDILVNP 287
DB 229 TWSRBATRSKTKLVVAVASPFILPLPQVGM-----MSFLBPSPPFLILNKL 281
QY 288 SSL-----AFNPSCLNPLLVFVQODFRERLIHSLPTSLERALSDSA-----PTND 334
DB 282 DSLCVSPAYINCINPIIYVAGGFGGRLRKSLPSLLRNLVTEBSVRSKSFTRSTVD 341
QY 335 TAA 337
DB 342 TMA 344

RESULT 9
S65766
G protein-coupled receptor (clone AZ3B) - human
C: Species: Homo sapiens (man)
C: Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C: Accession: S65766
R: Roglic, A.; Prossnitz, E.R.; Cavanagh, S.L.; Pan, Z.; Zou, A.; Ye, R.D.
Biochim. Biophys. Acta 1305, 39-43, 1996
A: Title: cDNA cloning of a novel G protein-coupled receptor with a large extracellular l
A: Reference number: S65766; MUID:96180983; PMID:8605247
A: Accession: S65766
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-482 <ROG>
A: Cross-references: UNIPROT:Q16581; UNIPARC:UPI0000126C11; EMBL:U28488; NID:91199577; PIR
C: Superfamily: vertebrate rhodopsin
C: Keywords: G protein-coupled receptor

Query Match 28.0%; Score 509.5; DB 2; Length 482;
Best Local Similarity 26.6%; Pred. No. 3.8e-35;
Matches 134; Conservative 59; Mismatches 117; Indels 193; Gaps 11;

QY 2 ETN-----FSRPLNYESVSYBSAGYTVLRILPLVVGTVFVLGNGLVIVVAGFRMTR 57
DB 7 ETNSTLLSOPNNEPPV-----ILSNVILSTFLGLPENGVLVWAGLKMQR 54
QY 58 TTTTTCYLMALADFSFTATLPPLIVSMAMGKMPGFWLCKLHIVVDINLFGSVFLIG 117
DB 55 TVNTIWFHLTLADLLCCSLPSLHNLALQGWGPGFRLCKLPSIILVNMPSAVFLIT 114
QY 118 FIALDRCICYLHNVAMQNHRTVSLANKVIVGPITLALVLTLPFLPLTTVTIINGDTCT 177
DB 115 AISLDRCLVLFKPIWQNHNVGMACSICGIVVAVFVWCIPVYVRBIFTTDNHR-CG 173
QY 178 FNA-----SW----- 183
DB 174 YKFGSSLDYDPFYDPLNLSLENIYQRPGRMDRLDPSSTQTDHPTVTFVQPOR 223
QY 184 -----GGTPEE-----R 190
DB 234 FORPSADSLPRGSARILSQNLVSNVFKPADVSPKIPSGPRIDHETPLDNDALFSTH 293
QY 191 LKV-----AIVMLTARGIIRFVIGSPISVIA 218
DB 294 LKLFPSASSNFYSESLPGQFDYVNLGQFTDDQVPTPLVATITIRLVVGFLLPSVIMI 353
QY 219 ICGILNAKIHKKMGLKS-SRPLRLTAVVASPFICMPFQVALLAGTWMKELFYGKY 277
DB 354 ACYSFTVFRQGRFPAKSKQTFRVAVVAVVLCWTPVH-----F 396
QY 278 KIIDILVNPTS-----SLAFNPSCLNPLLVFVQODFRERLIHSLPTSLER 323
DB 397 GVLSLTDPETPLGKILMSWDHVCILASANSFNFVIALGKDRKKARQSIGIILER 456
QY 324 ALSED-----SAPTNDTAANSAS 341
DB 457 AFSEELTRSTHCPSSNVVISERN 479

RESULT 10
JC5796
probable chemoattractant receptor - rat
C: Species: Rattus norvegicus (Norway rat)
C: Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C: Accession: JC5796
R: O'Leary, S.J.; Santen, S.; Olde, B.
Biochem. Biophys. Res. Commun. 241, 390-394, 1997
A: Title: Molecular cloning and tissue distribution of cDNA encoding a novel chemoattract
A: Reference number: JC5796; MUID:98086361; PMID:9425281
A: Accession: JC5796
A: Molecule type: mRNA
A: Residues: 1-371 <OMN>
A: Cross-references: UNIPROT:Q35786; UNIPARC:UPI0000127BD5; DBJ:AU002745; NID:g2624397; I

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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:10:33 ; Search time 277.992 Seconds

(without alignments)
890,819 Million cell updates/sec

Title: US-10-517-956-1

Perfect score: 1817

Sequence: 1 METNFTPTLNEYEVSYESA.....TNDTANASAPPAETIQAM 351

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1817	100.0	351	1 FPR1L_HUMAN	P25090 homo sapien
2	1782	98.1	348	1 FPR1L_PANTR	P79242 pan troglod
3	1781	98.0	348	1 FPR1L_GORGO	P79177 gorilla gor
4	1744	96.0	348	1 FPR1L_PONPY	P79236 pongo pygma
5	1740	95.8	348	1 FPR1L_MACMU	P79190 macaca mula
6	1420	78.2	351	2 O88536_MOUSE	O88536 mus musculu
7	1337	73.6	351	1 FPR1L_MOUSE	O08790 mus musculu
8	1327	73.0	353	2 O6L574_HUMAN	P25069 homo sapien
9	1327	73.0	353	2 O6L574_HUMAN	O6L574 homo sapien
10	1325	72.9	347	2 O88535_MOUSE	O88535 mus musculu
11	1312	72.2	349	1 FPR1L_PANTR	P79243 pan troglod
12	1304	71.8	349	1 FPR1L_PONPY	P79237 pongo pygma
13	1299	71.5	349	1 FPR1L_GORGO	P79178 gorilla gor
14	1292	71.1	349	1 FPR1L_MACMU	P79191 macaca mula
15	1243.5	68.4	350	1 FPR1L_HUMAN	P21462 homo sapien
16	1225.5	67.4	346	1 FPR1L_PANTR	P79241 pan troglod
17	1225.5	67.4	346	1 FPR1L_PONPY	P79235 pongo pygma
18	1223.5	67.3	352	1 FPR1L_RABIT	Q05394 oryctolagus
19	1206.5	66.4	346	1 FPR1L_GORGO	P79176 gorilla gor
20	1206.5	66.4	346	1 FPR1L_MACMU	P79189 macaca mula
21	1174.5	64.6	364	1 FPR1L_MOUSE	P73766 mus musculu
22	1140.5	62.8	343	2 O88537_MOUSE	O88537 mus musculu
23	1107.5	61.0	323	2 O88538_MOUSE	O88538 mus musculu
24	1074.5	59.1	338	2 Q71MK7_MOUSE	Q71MK7 mus musculu
25	1074.5	59.1	340	2 O8H290_SAGOB	O8H290 saguinus oe
26	1071.5	59.0	339	2 Q71MR8_MOUSE	Q71MR8 mus musculu
27	644	35.4	322	2 O4SMX3_TETNG	O4SMX3 tetradon n
28	585.5	32.2	322	2 O4RSY3_TETNG	O4RSY3 tetradon n
29	580.5	31.9	461	2 O5Z1N6_CHICK	O5Z1N6 gallus gall
30	553.5	30.5	356	1 GPR33_HUMAN	G75388 homo sapien
31	553.5	30.5	356	2 O502U7_HUMAN	O502U7 homo sapien

32	548.5	30.2	475	1 Q3AR_CANVO	O88680 cavia porce
33	543.5	29.9	356	2 Q6NWS5_HUMAN	Q6NWS5 homo sapien
34	542.5	29.9	477	1 Q3AR_MOUSE	Q09047 mus musculu
35	542.5	29.9	477	2 Q5U7A4_MOUSE	Q5U7A4 mus musculu
36	541.5	29.8	477	2 O8C6R2_MOUSE	O8C6R2 mus musculu
37	538.5	29.6	371	1 CML1_MOUSE	P97468 mus musculu
38	534.5	29.4	371	2 Q5U0H0_HUMAN	Q5U0H0 homo sapien
39	534.5	29.4	373	1 CML1_HUMAN	Q97768 homo sapien
40	530.5	29.2	382	1 GPR44_MOUSE	Q92236 mus musculu
41	530.5	29.2	382	2 Q54A00_MOUSE	Q54A00 mus musculu
42	530.5	29.2	473	1 Q3AR_RAT	O55197 rattus norv
43	513	28.2	350	1 C5AR_HUMAN	P21730 homo sapien
44	509.5	28.0	482	1 Q3AR_HUMAN	Q16581 homo sapien
45	509	28.0	403	2 Q6XKD3_RAT	Q6XKD3 rattus norv

ALIGNMENTS

RESULT 1	FPRL1_HUMAN	STANDARD;	PRT;	351 AA.
ID	FPRL1_HUMAN			
AC	P25090;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	FMPLP-related receptor I (FMPLP-R-I) (Lipoxin A4 receptor) (LXA4 receptor) (Formyl peptide receptor-like 1) (FPLP) (HM63).			
GN	Name=FPRL1; Synonyms=FPRL2, FPRH1, LXAAR;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=92307681; PubMed=1612600;			
RA	Bao L., Gerard N.P., Bddy R.L. Jr., Shows T.B., Gerard C.;			
RT	"Mapping of genes for the human C5a receptor (C5AR), human FMPLP receptor (FPR), and two FMPLP receptor homologue orphan receptors			
RT	(FPRH1, FPRH2) to chromosome 19.";			
RL	Genomics 13:437-440(1992).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Bone marrow;			
RX	MEDLINE=92360523; PubMed=1511907; DOI=10.1016/0378-1119(92)90208-7;			
RA	Perez H.D., Holmes R., Kelly B., McClary J., Andrews W.H.;			
RT	"Cloning of a cDNA encoding a receptor related to the formyl peptide			
RT	receptor of human neutrophils.";			
RL	Gene 118:303-304(1992).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Granulocyte;			
RX	MEDLINE=92246937; PubMed=1374236;			
RA	Ye R.D., Cavanagh S.L., Quehenberger O., Prossnitz E.R.;			
RT	Cochrane C.G.;			
RT	"Isolation of a cDNA that encodes a novel granulocyte N-formyl peptide			
RT	receptor.";			
RL	Biochem. Biophys. Res. Commun. 184:582-588(1992).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=92218423; PubMed=1373134;			
RA	Murphy P.M., Oseclik T., Kenney R.T., Tiffany H.L., McDermott D.;			
RT	Frankel U.;			
RT	"A structural homologue of the N-formyl peptide receptor.			
RT	Characterization and chromosome mapping of a peptide chemottractant			
RT	receptor family.";			
RL	J. Biol. Chem. 267:7637-7643(1992).			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Monocyte;			
RX	MEDLINE=94092629; PubMed=7505609;			
RA	Nomura H., Nielsen B.W., Matsushima K.;			

FT TOPO_DOM 307 351 Cytoplasmic (Potential).
 FT CARBOHYD 4 4 N-linked (GlcNAc...) (Potential).
 Query Match 100.0%; Score 1817; DB 1; Length 351;
 Best Local Similarity 100.0%; Pred. No. 1.6e-100;
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METNFTPLNEVEBESYESAGYTVLRILPLVLGVTFLVGLNGVLIVVAGFRMTRTVT 60
 DB 1 METNFTPLNEVEBESYESAGYTVLRILPLVLGVTFLVGLNGVLIVVAGFRMTRTVT 60
 QY 61 TICYNALADFSFTATLPFLIVSMAMGKMPGMLCKIHIYVDINLGSVPLGFIA 120
 DB 61 TICYNALADFSFTATLPFLIVSMAMGKMPGMLCKIHIYVDINLGSVPLGFIA 120
 QY 121 LDRICVLAHFVMAONHRTVSLAMKVIVGPMILVLTLPVPLFTVTITNGDTCYCFNF 180
 DB 121 LDRICVLAHFVMAONHRTVSLAMKVIVGPMILVLTLPVPLFTVTITNGDTCYCFNF 180
 QY 181 ASNGCTPEERLKAVALTMTLARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL 240
 DB 181 ASNGCTPEERLKAVALTMTLARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL 240
 QY 241 RVLTAVVASFICWPFQVALLGTWVKEMLFYGYKXIIDIIVNPTSSLAFFNSCLNPM 300
 DB 241 RVLTAVVASFICWPFQVALLGTWVKEMLFYGYKXIIDIIVNPTSSLAFFNSCLNPM 300
 QY 301 LVYFVGQDFRERLIHSLPTSLERLSEDSAPTNDTANASPPAETELQAM 351
 DB 301 LVYFVGQDFRERLIHSLPTSLERLSEDSAPTNDTANASPPAETELQAM 351

RESULT 2
 PPRL1 PANTR STANDARD; PRT; 348 AA.
 ID PPRL1 PANTR STANDARD; PRT; 348 AA.
 AC P79242;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FMLP-related receptor I (FMLP-R-I) (Fragment).
 GN Name=PPRL1;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Pan.
 NCBI_TaxID=9598;
 RN [1]
 RP NCBILOTIDE SEQUENCE.
 RX MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;
 RA Alvarez V., Coco E., Sehen F., Gonzalez-Koces S., Lopez-Larrea C.;
 RT "Molecular evolution of the N-formyl peptide and Csa receptors in non-
 human primates."; Immunogenetics 44:446-452(1996).
 RL Immunogenetics 44:446-452(1996).
 CC -1- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
 which are powerful neutrophils chemotactic factors. Binding of
 FMLP to the receptor causes activation of neutrophils. This
 response is mediated via a G-protein that activates a
 phosphatidylinositol-calcium second messenger system.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC EMBL: X97739; CA66323.1; -; Genomic_DNA.
 DR HSSP; P34996; 1DDP.
 DR InterPro; IPR000826; Frc/met_receptor.
 DR InterPro; IPR000276; GPCR_Rhodopn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00526; FMETLEUPHER.

DR PRINTS; PR00237; GPCR_RHODOPN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1;
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KM Chemotaxis; G-protein coupled receptor; Glycocalyx; Receptor;
 KM Sensory transduction; Transducer; Transmembrane.
 FT TOPO_DOM 348 348
 FT TRANSMEM 25 47
 FT TOPO_DOM 48 58
 FT TRANSMEM 59 80
 FT TOPO_DOM 81 97
 FT TRANSMEM 98 118
 FT TOPO_DOM 119 137
 FT TRANSMEM 138 159
 FT TOPO_DOM 160 202
 FT TRANSMEM 203 223
 FT TOPO_DOM 224 239
 FT TRANSMEM 240 263
 FT TOPO_DOM 264 283
 FT TRANSMEM 284 303
 FT TOPO_DOM 304 348
 FT CARBOHYD 1 1
 FT DISULFID 95 173
 FT NON_TER 1 1
 FT NON_TER 348 348
 SQ SEQUENCE 348 AA; 38575 MW; 55876670DF4D594E CRC64;
 Query Match 98.1%; Score 1782; DB 1; Length 348;
 Best Local Similarity 98.9%; Pred. No. 1.9e-98;
 Matches 344; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 NFSTPLNEVEBESYESAGYTVLRILPLVLGVTFLVGLNGVLIVVAGFRMTRTVTTC 63
 DB 1 NFSTPLNEVEBESYESAGYTVLRILPLVLGVTFLVGLNGVLIVVAGFRMTRTVTTC 60
 QY 64 YNTLALADFSFTATLPFLIVSMAMGKMPGMLCKIHIYVDINLGSVPLGFIALDR 123
 DB 64 YNTLALADFSFTATLPFLIVSMAMGKMPGMLCKIHIYVDINLGSVPLGFIALDR 120
 QY 124 CICALPVAONHRTVSLAMKVIVGPMILVLTLPVPLFTVTITNGDTCYCFNFASW 183
 DB 124 CICALPVAONHRTVSLAMKVIVGPMILVLTLPVPLFTVTITNGDTCYCFNFASW 180
 QY 184 GCTPEERLKAVALTMTLARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRV 243
 DB 184 GCTPEERLKAVALTMTLARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRV 240
 QY 244 TAVVASFICWPFQVALLGTWVKEMLFYGYKXIIDIIVNPTSSLAFFNSCLNPMKY 303
 DB 244 TAVVASFICWPFQVALLGTWVKEMLFYGYKXIIDIIVNPTSSLAFFNSCLNPMKY 300
 QY 304 FVGQDFRERLIHSLPTSLERLSEDSAPTNDTANASPPAETELQAM 351
 DB 304 FVGQDFRERLIHSLPTSLERLSEDSAPTNDTANASPPAETELQAM 348

RESULT 3
 PPRL1 GORGO STANDARD; PRT; 348 AA.
 ID PPRL1 GORGO STANDARD; PRT; 348 AA.
 AC P79177;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FMLP-related receptor I (FMLP-R-I) (Fragment).
 GN Name=PPRL1;
 OS Gorilla gorilla gorilla (Lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Gorilla.
 NCBI_TaxID=9595;
 RN [1]
 RP NCBILOTIDE SEQUENCE.
 RX MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;
 RA Alvarez V., Coco E., Sehen F., Gonzalez-Koces S., Lopez-Larrea C.;

```

RT "Molecular evolution of the N-formyl peptide and C5a receptors in non-
RT human primates."; 44:446-452(1996).
RL Immunogenetics 44:446-452(1996).
CC -1- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
CC which are powerful neutrophils chemotactic factors. Binding of
CC FMLP to the receptor causes activation of neutrophils. This
CC response is mediated via a G-protein that activates a
CC phosphatidylinositol-calcium second messenger system.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR HEMBL; X97738; CAA66322.1; -; Genomic_DNA.
DR HSP; P34996; 1DD.
DR InterPro; IPR000826; Frl/met_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00526; FMETLEUPHER.
DR PROSITE; PS00237; GPCR_HODOPSN.
DR PROSITE; PS00262; G_PROTEIN_REC_P1_1; 1.
KW Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor;
KW Sensory transduction; Transducer; Transmembrane.
FT TOPO_DOM <1 24
FT TRANSMEM 25 47
FT TOPO_DOM 48 58
FT TRANSMEM 59 80
FT TOPO_DOM 81 97
FT TRANSMEM 98 118
FT TOPO_DOM 119 137
FT TRANSMEM 138 159
FT TOPO_DOM 160 202
FT TRANSMEM 203 223
FT TOPO_DOM 224 239
FT TRANSMEM 240 263
FT TOPO_DOM 264 283
FT TRANSMEM 284 303
FT TOPO_DOM 304 348
FT CARBOHYD 1 1
FT DISULFID 95 173
FT NON_TER 1 1
FT SEQUENCE 348 AA; 38581 MW; B1P0B3BDC76CAA0 CRC64;
SQ
Query Match 98.0%; Score 1781; DB 1; Length 348;
Best Local Similarity 98.9%; Pred. No. 2.2e-98;
Matches 344; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 4 NFSTPLNBEVEVYESAGVTVLRILPLVVGVTFFVGLANGVIVVAGFRMRRTYTTIC 63
DB 1 NFSTPLNBEVEVYESAGVTVLRILPLVVGVTFFVGLANGVIVVAGFRMRRTYTTIC 60
QY 64 YNLALADSPFATLPFLIYSVMAMGKMPGWFCKLHIVVDINFGSVFLIGFTALDR 123
DB YNLALADSPFATLPFLIYSVMAMGKMPGWFCKLHIVVDINFGSVFLIGFTALDR 120
QY 124 CIGCVLHPVNAQNRRYTS/LAMKVIVGPMILALVITLPEVFLFTVITPNGDTYCTENFASW 183
DB CIGCVLHPVNAQNRRYTS/LAMKVIVGPMILALVITLPEVFLFTVITPNGDTYCTENFASW 180
QY 184 GGPBERLKVATIMLTPARGIIRFVIGPSLPMSTVAICVGI/IAKHKKGMKSSRPLRV 243
DB GGPBERLKVATIMLTPARGIIRFVIGPSLPMSTVAICVGI/IAKHKKGMKSSRPLRV 240
QY 244 TAVVASFFICMPFPQVALGLTVMLEKMLFYGKTKIIDILVNTSSLAFFNSCLANMLVY 303
DB TAVVASFFICMPFPQVALGLTVMLEKMLFYGKTKIIDILVNTSSLAFFNSCLANMLVY 300

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QY 304 FVGDPERLRILHSILPTSLERALSSEDAPNTDPAANSASPATELQAM 351
DB 301 FVGDPERLRILHSILPTSLERALSSEDAPNTDPAASCASPATELQAM 348
RESULT 4
ID FPRLL_PONPY STANDARD; PRT; 348 AA.
AC P79236;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FMLP-related receptor I (FMLP-R-I) (Fragment).
GN Name=FPRLL;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Pongo.
OC NCBI_TaxId=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;
RA Alvarez V., Coto B., Sehen F., Gouzaiek-Koces S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and C5a receptors in non-
human primates."; 44:446-452(1996).
RL Immunogenetics 44:446-452(1996).
CC -1- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
CC which are powerful neutrophils chemotactic factors. Binding of
CC FMLP to the receptor causes activation of neutrophils. This
CC response is mediated via a G-protein that activates a
CC phosphatidylinositol-calcium second messenger system.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR HEMBL; X97744; CAA66328.1; -; Genomic DNA.
DR InterPro; IPR000826; Frl/met_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00526; FMETLEUPHER.
DR PROSITE; PS00237; GPCR_HODOPSN.
DR PROSITE; PS00262; G_PROTEIN_REC_P1_1; 1.
KW Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor;
KW Sensory transduction; Transducer; Transmembrane.
FT TOPO_DOM <1 24
FT TRANSMEM 25 47
FT TOPO_DOM 48 58
FT TRANSMEM 59 80
FT TOPO_DOM 81 97
FT TRANSMEM 98 118
FT TOPO_DOM 119 137
FT TRANSMEM 138 159
FT TOPO_DOM 160 202
FT TRANSMEM 203 223
FT TOPO_DOM 224 239
FT TRANSMEM 240 263
FT TOPO_DOM 264 283
FT TRANSMEM 284 303
FT TOPO_DOM 304 348
FT CARBOHYD 1 1
FT DISULFID 95 173
FT NON_TER 1 1
FT SEQUENCE 348 AA; 38686 MW; E5A4D005CPA41616 CRC64;
SQ
Query Match 96.0%; Score 1744; DB 1; Length 348;
Best Local Similarity 96.6%; Pred. No. 3.5e-96;

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Matches 336; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 NFSTPLNEYEVSYESAGYTVLRILPLVVLGVTFLVGLNGVLVWAGFRMTRVTTTC 63
 1 NFSTPLNEYEVSYESAGYTVLRILPLVVLGVTFLVGLNGVLVWAGFRMTRVTTTC 60

QY 64 YLNLALADFSFTATLPFLIVSMANGKMPGFWFLCGLIHIVVDINFGSVFLIGFIALDR 123
 61 YLNLPLADFSFTATLPFLIVSMANGKMPGFWFLCGLIHIVVDINFGSVFLIGFIALDR 120

QY 124 CIGVLPVWVWQNRHTVSLAMKVIVGPMILAVLTVLPVPLFTVTTINGSDTYCFNFASW 183
 121 CIGVLPVWVWQNRHTVSLAMKVIVGPMILAVLTVLPVPLFTVTTINGSDTYCFNFASW 180

QY 184 GGTPEERLKVATITMLTARGIIRFVIGFSLPMSIYALCYGLIAAKIHKKGMKSSRPLRVL 243
 181 GGTPEERKVAITMLTARGIIRFVIGFSLPMSIYALCYGLIAAKIHKKGMKSSRPLRVL 240

QY 244 TAVVASFFTCWPFQVALLGTWVKEMLPYKTKIIDIIVNPTSSLAFFNSCLNPMLYV 303
 241 TAVVASFFTCWPFQVALLGTWVKEMLPYKTKIINIIVNPTSSLAFFNSCLNPMLYV 300

QY 304 FVGQDFRERLIHSLPTSLERALSDESAPTNDTANASPPAETELQAM 351
 301 FVGQDFRERLIHSLPTSLERALSDESAPTNDTANASPPAETELQAM 348

Db

RESULT 5

PPRL1 MACMU STANDARD; PRT; 348 AA.

ID PPRL1 MACMU STANDARD; PRT; 348 AA.

AC P79190;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FMLP-related receptor 1 (FMLP-R-1) (Fragment).
 GN Name=PPRL1;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecoinae; Macaca.
 NCBI_TaxID=9544;
 RN NCBIOTIDE SEQUENCE.
 RP MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;
 RA Alvarez V., Coco E., Shen P., Gonzalez-Koces S., Lopez-Larrea C.;
 RT "Molecular evolution of the N-formyl peptide and Csa receptors in non-
 human primates.";
 RL Immunogenetics 44:446-452(1996).
 CC -1- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
 which are powerful neutrophils chemotactic factors. Binding of
 FMLP to the receptor causes activation of neutrophils. This
 response is mediated via a G-protein that activates a
 phosphatidylinositol-calcium second messenger system.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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 use as long as its content is in no way modified and this statement is not
 removed.

CC EMBL: X97737; CAAG6321.1; -; Genomic_DNA.
 DR HSSP: P34996; 1DD.
 DR InterPro: IPR000826; Frc/met_receptor.
 DR InterPro: IPR000276; GPCR_Rhodpam.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00526; FMTLEUPHER.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KM Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor;
 Sensory transduction; Transducer; Transmembrane.

FT TOPO_DOM <1 24 Extracellular (Potential).
 FT TRANSHEM 25 47 1 (Potential).
 FT TOPO_DOM 48 58 Cytoplasmic (Potential).
 FT TRANSHEM 59 80 2 (Potential).
 FT TOPO_DOM 81 97 Extracellular (Potential).
 FT TRANSHEM 98 118 3 (Potential).
 FT TOPO_DOM 119 137 Cytoplasmic (Potential).
 FT TRANSHEM 138 159 4 (Potential).
 FT TOPO_DOM 160 202 Extracellular (Potential).
 FT TRANSHEM 203 223 5 (Potential).
 FT TOPO_DOM 224 239 Cytoplasmic (Potential).
 FT TRANSHEM 240 263 6 (Potential).
 FT TOPO_DOM 264 283 Extracellular (Potential).
 FT TRANSHEM 284 303 7 (Potential).
 FT TOPO_DOM 304 348 Cytoplasmic (Potential).
 FT CARBOHYD 1 1 N-linked (GlcNAc...) (Potential).
 FT DISULFID 95 173 Potential.
 FT NON_TER 1 1
 FT NON_TER 348 348
 SQ SEQUENCE 348 AA; 38457 MW; BC185DPAIC14B694E CRC64;

Query Match 95.8%; Score 1740; DB 1; Length 348;
 Best Local Similarity 96.6%; Pred. No. 6e-96;

Matches 336; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 4 NFSTPLNEYEVSYESAGYTVLRILPLVVLGVTFLVGLNGVLVWAGFRMTRVTTTC 63
 1 NFSTPLNEYEVSYESAGYTVLRILPLVVLGVTFLVGLNGVLVWAGFRMTRVTTTC 60

QY 64 YLNLALADFSFTATLPFLIVSMANGKMPGFWFLCGLIHIVVDINFGSVFLIGFIALDR 123
 61 YLNLALADFSFTATLPFLIVSMANGKMPGFWFLCGLIHIVVDINFGSVFLIGFIALDR 120

QY 124 CIGVLPVWVWQNRHTVSLAMKVIVGPMILAVLTVLPVPLFTVTTINGSDTYCFNFASW 183
 121 CIGVLPVWVWQNRHTVSLAMKVIVGPMILAVLTVLPVPLFTVTTINGSDTYCFNFASW 180

QY 184 GGTPEERLKVATITMLTARGIIRFVIGFSLPMSIYALCYGLIAAKIHKKGMKSSRPLRVL 243
 181 GGTPEERKVAITMLTARGIIRFVIGFSLPMSIYALCYGLIAAKIHKKGMKSSRPLRVL 240

QY 244 TAVVASFFTCWPFQVALLGTWVKEMLPYKTKIIDIIVNPTSSLAFFNSCLNPMLYV 303
 241 TAVVASFFTCWPFQVALLGTWVKEMLPYKTKIINIIVNPTSSLAFFNSCLNPMLYV 300

QY 304 FVGQDFRERLIHSLPTSLERALSDESAPTNDTANASPPAETELQAM 351
 301 FVGQDFRERLIHSLPTSLERALSDESAPTNDTANASPPAETELQAM 348

Db

RESULT 6

088536 MOUSE PRELIMINARY; PRT; 351 AA.

ID 088536; PRT; 351 AA.

AC 088536;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE N-formylpeptide receptor-like 2 (Npoxin A4 receptor-like
 protein).
 GN Name=Fpr-1a2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN NCBIOTIDE SEQUENCE.
 RP MEDLINE=98390190; PubMed=9722950; DOI=10.1006/geno.1998.5376;
 RA Gao J.-L., Chen H., Fille J.D., Kozak C.A., Murphy P.M.;
 RT "Differential expansion of the N-formylpeptide receptor gene cluster
 in human and mouse.";
 RL Genomics 51:270-276(1998).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN-B10.A;
RX MEDLINE=22206880; PubMed=12218158;
RA Vaughn M.W., Proske R.J., Haviland D.L.;
RT "identification, cloning, and functional
RT lipoxin A4 receptor homologue gene.";
RL J. Immunol. 169:3363-3369(2002).
RR EMBL; AF071180; AAC34585.1; -; Genomic DNA.
DR EMBL; AY138248; AAC06932.1; -; Genomic DNA.
DR Ensembl; ENSMG00000052270; Mus musculus.
MG1; MGI:1278319; Pdx-rs2.
DR GO; GO:0004872; F:receptor activity; IDA.
DR InterPro; IPR001644; C3anrx_receptor.
DR InterPro; IPR000826; FcR/met_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01060; C3ANPHYLTNKR.
DR PRINTS; PR00526; FMETLEUPHER.
DR PRINTS; PR00237; GPCR RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; UNKNOWN_1.
DR PROSITE; PS02062; G_PROTEIN_REC_P1_2; 1.
KM Receptor.
SQ SEQUENCE 351 AA; 39422 MW; B16BCETP9A9AF43 CRC64;

Query Match	Similarity	76.3%	Score 1420	DB 2	Length 351
Best Local	Similarity	76.3%	Pred. No. 6,6e-77		
Matches 267	Conservative	33	Mismatches 50	Indels 0	Gaps 0

Query	1	MEINSTEPLNVEBVSYSAGYTVLRILPLVVLGVTPLVGLVGNLVIWVAGFRMTRTYT	60
Db	1	MESNYSIHLSNSEVVVDYDSTISRVLMIISMVVSITFFLGVGLGNGLVIWVAGFRMTRTYT	60
Qy	61	TTCITLNLALAPSPFATPLPLILVSNAMKEKPPGFFLCKLHIWVDIMLFGSVFLIGTIA	120
Db	61	TIWYINLALADFSFATPLPLILVSNAMKEKPPGFFLCKLHIWVDIMLFGSVFLIGTIA	120
Qy	121	LDRICICVLHPVMAQNRHTVSLAMKIVGPMILALVLTLPVPLFTLTVTIIPGDDVCTENF	180
Db	121	LDRICICVLHPVMAQNRHTVSLARKKVQWPMIFALTLPIFTLTVTIIPGDDVCTENF	180
Qy	181	ASMGTPPEERLKVATIMLTARGIIRFVIGFSLPMSIVAICYGLIAKIHKKMIKSRPL	240
Db	181	GSMAGTDEKRLNTAIFFTTGRGIRFLGFSMPMSIVAQGLIAVKINRNLVNSSRPL	240
Qy	241	RLVLAIVVASPFTICMPFFPOLVALLGTWMLKEMLPFGKXIIDILNPFSSLAFFNSCLNPM	300
Db	241	RLVLAIVVASPFTICMPFFPOLVALLGTWMLKEMLPFGKXIIDILNPFSSLAFFNSCLNPM	300
Qy	301	LYVAVGDFRERLHSLPTSLERALSBSAPLNDPAAASAPPAETLQIA	350
Db	301	LYVAVGDFRERLHSLPTSLERALSBSGGSSTSPSPADIEKIA	350

RESULT 7	FPRL1 MOUSE	STANDARD	PRT	351 AA
AC	008790			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	FMPL-related receptor I (FMPL-R-I) (Lipoxin A4 receptor) (LXA4 receptor)			
GN	Name=Fpr1l; Synonym=Ixa4r;			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muridea; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	NCLECTIDE SEQUENCE.			
RC	TISSUE=Neutrophil, and Spleen;			
RX	MEDLINE=97296322; PubMed=9151906; DOI=10.1084/jem.185.9.1693;			
RA	Takano T., Fiore S., Maddox J.F., Brady H.R., Petasis N.A.,			

RA Serhan C.N.;
RT "Acap1in-1-triggered 15-epi-lipoxin A4 (LXA4) and LXA4 stable analogues
RT are potent inhibitors of acute inflammation: evidence for anti-
RT inflammatory receptors";
RL J. Exp. Med. 185:1693-1704 (1997).
CC -1- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
CC which are powerful neutrophils chemotactic factors. Binding of
CC FMLP to the receptor causes activation of neutrophils. This
CC response is mediated via a G-protein that activates a
CC phosphatidylinositol-calcium second messenger system. The
CC activation of LXA4r could result in an anti-inflammatory outcome
CC connecting the actions of proinflammatory signals such as LTB4
CC (leukotriene B4).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed mostly in neutrophils, followed by
CC spleen and lung. Expressed at very low levels in heart and liver.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

[illegible]

QY 121 LDRICVYLHPVMAQNHRTVSLAMKVIVPMTIALVLTLPVPLFTVTVTPNGDYCTENF 180
 DB 121 LDRICVYLHPVMAQNHRTVSLAMKVIVPMTIALVLTLPVPLFTVTVTPNGDYCTENF 180
 QY 181 ASMGCTEERELKVAITMLTARGIRFVYFSLPMSIYACVGLIAAKIHKMKIKSRPL 240
 DB 181 VSMGNSVEERLNTMTITVTTRIGIRFVYFSLPMSIYACVGLIAAKIHKMKIKSRPL 240
 QY 241 RVLTAVASFFICMPFQVALLGTVLWKEMLFYKXKIIDILVNPSTSLAFNSCLNPM 300
 DB 241 RVLTAVASFFICMPFQVALLGTVLWKEMLFYKXKIIDILVNPSTSLAFNSCLNPM 300
 QY 301 LYPVGVGDPRRRLHSLPTSLERLSRDSAPTNTAANSKSPPEKTLQOM 351
 DB 301 LYPVGVGDPRRRLHSLPTSLERLSRDSAPTNTAANSKSPPEKTLQOM 351
 RESULT 8
 PPRL2_HUMAN STANDARD; PRT; 353 AA.
 AC P25089;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FMLP-related receptor, II (FMLP-R-II) (Formylpeptide receptor-like 2).
 GN Name=PPRL2; Synonym=PPRL1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo
 NCBI_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=92307681; Pubmed=1612600;
 RA Bao L., Gerard N.P., Bddy R.L. Jr., Shows T.B., Gerard C.;
 RT "Mapping of genes for the human C5a receptor (C5AR), human FMLP
 receptor (FPR), and two FMLP receptor homologue orphan receptors
 (PPRL1, PPRL2) to chromosome 19.";
 RL Genomics 13:437-440 (1992).
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=94256976; Pubmed=8198572;
 RA Durstun M., Gao J.-L., Tiliaty H.L., McDermott D., Murphy P.M.;
 RT "Differential expression of members of the N-formylpeptide receptor
 gene cluster in human phagocytes.";
 RL Biochem. Biophys. Res. Commun. 201:174-179 (1994).
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP Kopatz S.A., Aronstam R.S., Shatma S.V.;
 RA "cDNA clones of human proteins involved in signal transduction
 sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heide F.,
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lonnell N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hultk S.W.,
 RA Villion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hulton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Buttefield Y.S.N., Krzywinski M.I., Skalek U., Smallins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
 CC which are powerful neutrophil chemotactic factors. Binding of
 CC FMLP to the receptor causes activation of neutrophils. This
 CC response is mediated via a G-protein that activates a
 CC phosphatidylinositol-calcium second messenger system.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 DR EMBL: M76673; AA58487.1; -; mRNA.
 DR EMBL: L14061; AA52474.1; -; Genomic DNA.
 DR EMBL: AY262690; AAP20654.1; -; Genomic DNA.
 DR EMBL: BC059388; AAH59388.1; -; mRNA.
 DR EMBL: BC069070; AAH69070.1; -; mRNA.
 DR EMBL: BC069593; AAH69593.1; -; mRNA.
 DR EMBL: BC069812; AAH69812.1; -; mRNA.
 DR FTR: C42009; C42009.
 DR Ensembl: ENSG00000187474; Homo sapiens.
 DR HGNC: HGNC:3828; PPRL2.
 DR MIM: 136539; -;
 DR GO: GO:0016021; C: integral to membrane; TAS.
 DR GO: GO:0005886; C: plasma membrane; TAS.
 DR GO: GO:0004982; F: N-formyl peptide receptor activity; TAS.
 DR GO: GO:0006928; P: cell motility; TAS.
 DR GO: GO:0007165; P: signal transduction; TAS.
 DR InterPro: IPR000826; Ftr/met receptor.
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1, 1.
 DR PRINTS: PR00526; FMETLUPHER.
 DR PRINTS: PR00237; GPCRHOPOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS02652; G_PROTEIN_RECEP_F1_2; 1.
 KW Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor;
 KW Sensory transduction; Transducer; Transmembrane.
 FT TOPO_DOM 1 27
 FT TRANSMEM 28 50
 FT TOPO_DOM 51 61
 FT TRANSMEM 62 83
 FT TOPO_DOM 84 100
 FT TRANSMEM 101 121
 FT TOPO_DOM 122 140
 FT TRANSMEM 141 162
 FT TOPO_DOM 163 205
 FT TRANSMEM 206 226
 FT TOPO_DOM 227 242
 FT TRANSMEM 243 266
 FT TOPO_DOM 267 286
 FT TRANSMEM 287 306
 FT TOPO_DOM 307 353
 FT CARBOHYD 4 4
 FT CARBOHYD 10 10
 FT DISULFID 98 176
 FT CONFLICT 94 94
 FT CONFLICT 211 211
 FT CONFLICT 338 338
 SQ SEQUENCE 353 AA; 39965 MW; FFB7150B6A833F4C CRC64;
 Query Match 73.0%; Score 1327; DB 1; Length 353;
 Best Local Similarity 72.2%; Pred. No. 2,3e-71;
 Matches 255; Conservative 38; Mismatches 58; Indels 2; Gaps 1;
 QY 1 MENTSTPLNBYEVSYSAGTYVRLPLVVLGTYFVGUGNGVYVAGPRMRTTY 60
 DB 1 METNFSIPLNTEBEVLPBPAQHTVLMIFSLVLHGVTFFVGVLGNGVIVVAGPRMRTTY 60

QY 61 TTYLNLALADSFATLPLIYSMANGKPGWFLCKLHIVVDINLFGSVFLIGFIA 120
 DB 61 TTYLNLALADSFATLPLIYSMANGKPGWFLCKLHIVVDINLFGSVFLIGFIA 120
 QY 121 LDRICIVLHPVMAQNHRVTSIAKVIYGVPIALVLTLPVFLPTVTTIPNGDTYCTFNF 180
 DB 121 LDRICIVLHPVMAQNHRVTSIAKVIYGVPIALVLTLPVFLPTVTTIPNGDTYCTFNF 180
 QY 181 ASWGTPPEERLKYAITMLTARGIIRFVIGSLPMSIACVGLIAKHKMKIKSRPL 240
 DB 181 ASWGTPPEERLKYAITMLTARGIIRFVIGSLPMSIACVGLIAKHKMKIKSRPL 240
 QY 241 RUTAVAVASFFICWPPFQVALLGTWMLKEMLFYGYKKIIDIIVNPSSIAFNSCLNPM 300
 DB 241 RUTAVAVASFFICWPPFQVALLGTWMLKEMLFYGYKKIIDIIVNPSSIAFNSCLNPM 300
 QY 301 LVYFVGODPFRRLIHSLSPTSLERALS--DSAPTPNDPAANSASPATELQAM 351
 DB 301 LVYFVGODPFRRLIHSLSPTSLERALS--DSAPTPNDPAANSASPATELQAM 351

RESULT 9
 ID 061534_HUMAN PRELIMINARY; PRT; 353 AA.
 AC 061534;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE FHL2_HUMAN.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lameddin J.B., McCreedy P.M., Skowronski E., Vismannathan V.,
 RA Burkhart-Schultze K.J., Brower A., Gordon L., Diaz J., Ramirez M.,
 RA Stillwagen S., Phan H., Velasco N., Do L., Regala W., Terry A.,
 RA Garner J., Danganan L., Erler A., Christensen M., Georgescu A.,
 RA Avila J., Liu S., Atlix C., Andrae S., Lucas S., Bruce R.,
 RA Amico-Keller G., Coefield J., Darte S., Lucas S., Bruce R.,
 RA Thomas P., Quan G., Krommiller B., Arellano A., Sanders C., Ow D.,
 RA Nolan M., Truong S., Kobayashi A., Olsen A.S., Carraro A.V.,
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 SM EMBL:AC005946; AAC72102.1; -; Genomic DNA.
 SQ SEQUENCE 353 AA; 39965 MW; FFB150B6A833F4C CRC64;

Query Match 73.0%; Score 1327; DB 2; Length 353;
 Best Local Similarity 72.2%; Pred. No. 2.3e-71;
 Matches 255; Conservative 38; Mismatches 58; Indels 2; Gaps 1;
 QY 1 METNFTPIINYEVEVSAGYTVLRILPLVVGTVFVGLVNGLVYVWAGFRMRTYT 60
 DB 1 METNFTPIINYEVEVSAGYTVLRILPLVVGTVFVGLVNGLVYVWAGFRMRTYT 60
 QY 61 TTYLNLALADSFATLPLIYSMANGKPGWFLCKLHIVVDINLFGSVFLIGFIA 120
 DB 61 TTYLNLALADSFATLPLIYSMANGKPGWFLCKLHIVVDINLFGSVFLIGFIA 120
 QY 121 LDRICIVLHPVMAQNHRVTSIAKVIYGVPIALVLTLPVFLPTVTTIPNGDTYCTFNF 180
 DB 121 LDRICIVLHPVMAQNHRVTSIAKVIYGVPIALVLTLPVFLPTVTTIPNGDTYCTFNF 180
 QY 181 ASWGTPPEERLKYAITMLTARGIIRFVIGSLPMSIACVGLIAKHKMKIKSRPL 240
 DB 181 ASWGTPPEERLKYAITMLTARGIIRFVIGSLPMSIACVGLIAKHKMKIKSRPL 240
 QY 241 RUTAVAVASFFICWPPFQVALLGTWMLKEMLFYGYKKIIDIIVNPSSIAFNSCLNPM 300
 DB 241 RUTAVAVASFFICWPPFQVALLGTWMLKEMLFYGYKKIIDIIVNPSSIAFNSCLNPM 300
 QY 301 LVYFVGODPFRRLIHSLSPTSLERALS--DSAPTPNDPAANSASPATELQAM 351
 DB 301 LVYFVGODPFRRLIHSLSPTSLERALS--DSAPTPNDPAANSASPATELQAM 351

DB 301 LVYFVGODPFRRLIHSLSPTSLERALS--DSAPTPNDPAANSASPATELQAM 353

RESULT 10
 ID 088535_MOUSE PRELIMINARY; PRT; 347 AA.
 AC 088535;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE N-formylpeptide receptor-like 1.
 GN Name=Fpr-1a;
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE:98390190; PubMed:9722950; DOI=10.1006/geno.1998.5376;
 RA Gao J.-L., Chen H., Fille J.D., Kozak C.A., Murphy P.M.;
 RT "Differential expansion of the N-formylpeptide receptor gene cluster
 in human and mouse."
 RU Genomics 51:270-276(1998).
 RL EMBL:AF071179; AAC34584.1; -; Genomic DNA.
 DR Ensembl:ENSMUSG0000052270; Mus musculus.
 DR MGI:MGI:1278320; Fpr-1a.
 DR GO:GO:0016021; C:integral to membrane; IEA.
 DR GO:GO:0004982; P:N-formyl peptide receptor activity; IEA.
 DR GO:GO:0004872; P:receptor activity; IEA.
 DR GO:GO:0001584; P:rhodopsin-like receptor activity; IEA.
 DR GO:GO:007186; P:G-protein coupled receptor protein signaln. . .; IEA.
 DR InterPro:IPR001644; C3aAnx_receptor.
 DR InterPro:IPR000826; Fpr/met_receptor.
 DR InterPro:IPR000276; GPCR_rhodopsn.
 DR Pfam:PF00001; 7tm1.1.
 DR PRINTS:PRO1060; C3ANPHYLYXNR.
 DR PRINTS:PRO0526; FMYLIEUPHER.
 DR PRINTS:PRO0237; GPCRHHODPSN.
 DR PROSITE:PS00237; G PROTEIN RECP F1.1; UNKNOWN_1.
 DR PROSITE:PS0262; G_PROTEIN_RECPEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 347 AA; 39071 MW; A755BF9P09575A70 CRC64;

Query Match 72.9%; Score 1325; DB 2; Length 347;
 Best Local Similarity 73.2%; Pred. No. 2.9e-71;
 Matches 257; Conservative 27; Mismatches 63; Indels 4; Gaps 1;
 QY 1 METNFTPIINYEVEVSAGYTVLRILPLVVGTVFVGLVNGLVYVWAGFRMRTYT 60
 DB 1 METNFTPIINYEVEVSAGYTVLRILPLVVGTVFVGLVNGLVYVWAGFRMRTYT 60
 QY 61 TTYLNLALADSFATLPLIYSMANGKPGWFLCKLHIVVDINLFGSVFLIGFIA 120
 DB 61 TTYLNLALADSFATLPLIYSMANGKPGWFLCKLHIVVDINLFGSVFLIGFIA 120
 QY 121 LDRICIVLHPVMAQNHRVTSIAKVIYGVPIALVLTLPVFLPTVTTIPNGDTYCTFNF 180
 DB 121 LDRICIVLHPVMAQNHRVTSIAKVIYGVPIALVLTLPVFLPTVTTIPNGDTYCTFNF 180
 QY 181 ASWGTPPEERLKYAITMLTARGIIRFVIGSLPMSIACVGLIAKHKMKIKSRPL 240
 DB 181 ASWGTPPEERLKYAITMLTARGIIRFVIGSLPMSIACVGLIAKHKMKIKSRPL 240
 QY 241 RUTAVAVASFFICWPPFQVALLGTWMLKEMLFYGYKKIIDIIVNPSSIAFNSCLNPM 300
 DB 241 RUTAVAVASFFICWPPFQVALLGTWMLKEMLFYGYKKIIDIIVNPSSIAFNSCLNPM 300
 QY 301 LVYFVGODPFRRLIHSLSPTSLERALS--DSAPTPNDPAANSASPATELQAM 351
 DB 301 LVYFVGODPFRRLIHSLSPTSLERALS--DSAPTPNDPAANSASPATELQAM 351

```

RESULT 11
PRL2_PANTR STANDARD; PRT; 349 AA.
ID PRL2_PANTR STANDARD; PRT; 349 AA.
AC P79243;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FMLP-related receptor II (FMLP-R-II) (Formylpeptide receptor-like 2)
DE (Fragment).
GN Name=FRL2;
OS Pan troglodytes (Chimpanzee).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Pan.
OC NCBI_TaxID=9598;
RN NCBI_TaxID=9598;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;
RA Alvarez V., Coco E., Sehén F., Gonzalez-Koces S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and C5a receptors in non-
RT human primates.";
RL Immunogenetics 44:446-452(1996).
CC -I- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
CC which are powerful neutrophils chemotactic factors. Binding of
CC FMLP to the receptor causes activation of neutrophils. This
CC response is mediated via a G-protein that activates a
CC phosphatidylinositol-calcium second messenger system.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X97743; CA66327.1; -; Genomic DNA.
CC InterPro: IPR000826; Frl/met receptor.
CC InterPro: IPR00276; GPCR_Rhodopsin.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS; PRO0526; FMTLEUPHER.
CC PROSITE; PS00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECPT_F2_1; 1.
CC Chemotaxis; G-protein coupled receptor; Glycopoltein; Receptor;
CC Sensory transduction; Transducer; Transmembrane.
CC TOPO_DOM 1 27
CC Transmem 1 (Potential).
CC Transmem 51 61
CC Transmem 62 83
CC Transmem 84 100
CC Transmem 101 121
CC Transmem 122 140
CC Transmem 141 162
CC Transmem 163 205
CC Transmem 206 226
CC Transmem 227 242
CC Transmem 243 266
CC Transmem 267 286
CC Transmem 287 306
CC TOPO_DOM 307 >349
CC CARBOHYD 4 4
CC CARBOHYD 10 10
CC DISULFID 98 176
CC NON_TER 349 349
CC SEQUNCE 349 AA; 39611 MW; 88279F8C72915383 CRC64;

Query Match 72.2%; Score 1312; DB 1; Length 349;
Best Local Similarity 72.2%; Pred. No. 1.7e-7;
Matches 252; Conservative 37; Mismatches 58; Indels 2; Gaps 1;
QY 1 METNFSITPLNEBVEBSYASGYTVLRILPLVLGVTFVLGVLGGLVIVWAGFRMTTIVT 60

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Db 1 METNFSITPLNEBVEBSYASGYTVLRILPLVLGVTFVLGVLGGLVIVWAGFRMTTIVT 60
QY 61 TICYINMALADSFATLPLFLIVSMAGKMPGFLCKLIHIVDINFGSVFLIGFLA 120
Db 61 TICYINMALADSFATLPLFLIVSMAGKMPGFLCKLIHIVDINFGSVFLIGFLA 120
QY 121 LDRICIVLHPWAQNRTYSLAMKVIVGPMITLALVTLTPVFLPLTVTIENGDTCTPNE 180
Db 121 LDRICIVLHPWAQNRTYSLAMKVIVGPMITLALVTLTPVFLPLTVTIENGDTCTPNE 180
QY 181 ASWGTPERLRKATIMLARGIIRFVIGFSLPMSIVACYGLIAKHKKMKSSRPL 240
Db 181 ASWGTPERLRKATIMLARGIIRFVIGFSLPMSIVACYGLIAKHKKMKSSRPL 240
QY 241 RVLTAIVASFFICFPFQVALVGLTWLKMELFYGRKTIIDILVNTSSLAFFNSCLNPM 300
Db 241 RVLTAIVASFFICFPFQVALVGLTWLKMELFYGRKTIIDILVNTSSLAFFNSCLNPM 300
QY 301 LYFVQODRERLHSLPISLEALSE--DSAPTNDTANASAPPATE 347
Db 301 LYFVQODRERLHSLPISLEALSE--DSAPTNDTANASAPPATE 347
QY 301 LYFVQODRERLHSLPISLEALSE--DSAPTNDTANASAPPATE 347
Db 301 LYFVQODRERLHSLPISLEALSE--DSAPTNDTANASAPPATE 347

RESULT 12
PRL2_PONPY STANDARD; PRT; 349 AA.
ID PRL2_PONPY STANDARD; PRT; 349 AA.
AC P79237;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FMLP-related receptor II (FMLP-R-II) (Formylpeptide receptor-like 2)
DE (Fragment).
GN Name=FRL2;
OS Pongo pygmaeus (Orangutan).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Pongo.
OC NCBI_TaxID=9600;
RN NCBI_TaxID=9600;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;
RA Alvarez V., Coco E., Sehén F., Gonzalez-Koces S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and C5a receptors in non-
RT human primates.";
RL Immunogenetics 44:446-452(1996).
CC -I- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
CC which are powerful neutrophils chemotactic factors. Binding of
CC FMLP to the receptor causes activation of neutrophils. This
CC response is mediated via a G-protein that activates a
CC phosphatidylinositol-calcium second messenger system.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X97741; CA66325.1; -; Genomic DNA.
CC InterPro: IPR000826; Frl/met receptor.
CC InterPro: IPR00276; GPCR_Rhodopsin.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS; PRO0526; FMTLEUPHER.
CC PROSITE; PS00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECPT_F2_1; 1.
CC Chemotaxis; G-protein coupled receptor; Glycopoltein; Receptor;
CC Sensory transduction; Transducer; Transmembrane.
CC TOPO_DOM 1 27
CC Transmem 28 50
CC Transmem 51 61
CC TOPO_DOM 51 61
CC Cytoplasmic (Potential).

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FT TRANSMEM 62 83 2 (Potential).
FT TOPO_DOM 84 100 Extracellular (Potential).
FT TRANSMEM 101 121 3 (Potential).
FT TOPO_DOM 122 140 Cytoplasmic (Potential).
FT TRANSMEM 141 162 4 (Potential).
FT TOPO_DOM 163 205 Extracellular (Potential).
FT TRANSMEM 206 226 5 (Potential).
FT TOPO_DOM 227 242 Cytoplasmic (Potential).
FT TRANSMEM 243 266 6 (Potential).
FT TOPO_DOM 267 286 Extracellular (Potential).
FT TRANSMEM 287 306 7 (Potential).
FT TOPO_DOM 307 >349 Cytoplasmic (Potential).
FT CARBOHYD 4 4 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 10 10 N-linked (GlcNAc...) (Potential).
FT DISULFID 98 176 Potential.
FT NON_TER 349 349
SQ SEQUENCE 349 AA; 39424 MW; C8298D223395EBC8 CRC64;

Query Match 71.8%; Score 1304; DB 1; Length 349;
Best Local Similarity 71.6%; Pred. No. 5.2e-70;
Matches 250; Conservative 39; Mismatches 58; Indels 2; Gaps 1;

QY 1 METNFTPLNREYSEVSAGYTVLRILPLVVGTVFVLGNGLVTVWAGFRMTRTVT 60
DB 1 METNFTPLNRESEVLPBPAGHTVLMIFSLVHGVTIFGVGNGLVWAGFRMTRTVN 60
QY 61 TICYNLMALADFSFTATLPPLIVSMAMGEKMPFGFLCKLHIIVVDINLFGSVFLIGFLA 120
DB 61 TICYNLMALADFSFSAIPLPFWVSVAMREKMPGTFLCKLVHMIDINLFGSVYLLITIA 120
QY 121 LDRICICVLPWAAQNRHTVSLAMKVIYGPWIALVLTLPVFLTVTVITPNQDTCTNF 180
DB 121 LDRICICVLPWAAQNRHTVSLAMKVIYGPWIALVLTLPVFLTVTVITPNQDTCTNF 180
QY 121 LDRICICVLPWAAQNRHTVSLAMKVIYGPWIALVLTLPVFLTVTVITPNQDTCTNF 180
DB 121 LDRICICVLPWAAQNRHTVSLAMKVIYGPWIALVLTLPVFLTVTVITPNQDTCTNF 180
QY 181 ASNGGTPEERLKVATITMLTARGIIRFVIGFSLPMSIIVACGLIAKIHKKMKISRP 240
DB 181 PFGGDTAVERLNVITMAKVFILHFIIGFSMPMSIITVYCGIIAKIHRNMIKSSRP 240
QY 241 RVLTAIVVASFPIQWPFQVALLGTVMLKEMLFYQKIKIIDLVPNTSSLAFFNSCLNPM 300
DB 241 RVLTAIVVASFPIQWPFQVALLGTVMLKEMLFYQKIKIIDLVPNTSSLAFFNSCLNPM 300
QY 301 LYFVPGDPRERLIHSLPISLERALSE--DSAPNTDITANSASPAPETE 347
DB 301 LYFVPGDPRERLIHSLPISLERALTEVPDSQTSNHTTSASPAPETE 349

RESULT 13
FPR12_GORGO STANDARD; PRT; 349 AA.
ID FPR12_GORGO
AC P79178;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FMLP-related receptor II (FMLP-R-II) (Formylpeptide receptor-like 2)
DE (Fragment).
GN Name=FPR12;
OS Gorilla gorilla gorilla (lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Gorilla.
OX NCBI_TaxID=9595;
RN (1)
RX NUCLEOTIDE SEQUENCE.
RP MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;
RA Alvarez V., Coco E., Sehen F., Gonzalez-Kocce S., Lopez-Larrea C.;
RT "Molecular evolution of the N-formyl peptide and Csa receptors in non-
human primates.";
RL Immunogenetics 44:446-452(1996).
CC -I- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
CC which are powerful neutrophil chemotactic factors. Binding of
CC FMLP to the receptor causes activation of neutrophils. This
CC response is mediated via a G-protein that activates a

```

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CC phosphatidylinositol-calcium second messenger system.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL: X97742; CAA6326.1; -; Genomic DNA.
DR InterPro: IPR000826; Ftr/met_receptor.
DR InterPro: IPR00276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00526; FMETLEUPHER.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor;
KW Sensory transduction; Transducer; Transmembrane.
FT TOPO_DOM 1 27 Extracellular (Potential).
FT TRANSMEM 28 50 1 (Potential).
FT TOPO_DOM 51 61 Cytoplasmic (Potential).
FT TRANSMEM 62 83 2 (Potential).
FT TOPO_DOM 84 100 Extracellular (Potential).
FT TRANSMEM 101 121 3 (Potential).
FT TOPO_DOM 122 140 Cytoplasmic (Potential).
FT TRANSMEM 141 162 4 (Potential).
FT TOPO_DOM 163 205 Extracellular (Potential).
FT TRANSMEM 206 226 5 (Potential).
FT TOPO_DOM 227 242 Cytoplasmic (Potential).
FT TRANSMEM 243 266 6 (Potential).
FT TOPO_DOM 267 286 Extracellular (Potential).
FT TRANSMEM 287 306 7 (Potential).
FT TOPO_DOM 307 >349 Cytoplasmic (Potential).
FT CARBOHYD 4 4 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 10 10 N-linked (GlcNAc...) (Potential).
FT DISULFID 98 176 Potential.
FT NON_TER 349 349
SQ SEQUENCE 349 AA; 39433 MW; C6BD77CFDE023834 CRC64;

Query Match 71.5%; Score 1299; DB 1; Length 349;
Best Local Similarity 71.3%; Pred. No. 1e-69;
Matches 249; Conservative 38; Mismatches 60; Indels 2; Gaps 1;

QY 1 METNFTPLNREYSEVSAGYTVLRILPLVVGTVFVLGNGLVTVWAGFRMTRTVT 60
DB 1 METNFTPLNRESEVLPBPAGHTVLMIFSLVHGVTIFGVGNGLVWAGFRMTRTVN 60
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DB 61 TICYNLMALADFSFSAIPLPFWVSVAMREKMPFGFLCKLVHMIDINLFGSVYLLITIA 120
QY 121 LDRICICVLPWAAQNRHTVSLAMKVIYGPWIALVLTLPVFLTVTVITPNQDTCTNF 180
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QY 121 LDRICICVLPWAAQNRHTVSLAMKVIYGPWIALVLTLPVFLTVTVITPNQDTCTNF 180
DB 121 LDRICICVLPWAAQNRHTVSLAMKVIYGPWIALVLTLPVFLTVTVITPNQDTCTNF 180
QY 181 ASNGGTPEERLKVATITMLTARGIIRFVIGFSLPMSIIVACGLIAKIHKKMKISRP 240
DB 181 PFGGDTAVERLNVITMAKVFILHFIIGFSMPMSIITVYCGIIAKIHRNMIKSSRP 240
QY 241 RVLTAIVVASFPIQWPFQVALLGTVMLKEMLFYQKIKIIDLVPNTSSLAFFNSCLNPM 300
DB 241 RVLTAIVVASFPIQWPFQVALLGTVMLKEMLFYQKIKIIDLVPNTSSLAFFNSCLNPM 300
QY 301 LYFVPGDPRERLIHSLPISLERALSE--DSAPNTDITANSASPAPETE 347
DB 301 LYFVPGDPRERLIHSLPISLERALTEVPDSQTSNHTTSASPAPETE 349

RESULT 14
FPR12_MACMU STANDARD; PRT; 349 AA.
ID FPR12_MACMU

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AC P79191;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE FMLP-related receptor II (FMLP-R-II) (Formylpeptide receptor-like 2) (Fragment).
 GN Name=PPRL2;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecoidea; Cercopithecoidea; Macaca.
 NC NCBI_TaxID=9544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;
 RA Alvarez V., Coto E., Shen F., Gonzalez-Koces S., Lopez-Larrea C.;
 RT "Molecular evolution of the N-formyl peptide and C5a receptors in non-human primates".
 RL Immunogenetics 44:446-452(1996).
 CC -I- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides, which are powerful neutrophils chemotactic factors. Binding of FMLP to the receptor causes activation of neutrophils. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 DR EMBL: X97740; CAA66324.1; -; Genomic DNA.
 DR InterPro: IPR000826; FRC/mec_receptor.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00526; FMETLEUPHER.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE: PS00262; G-PROTEIN RECP_F1_2; 1.
 DR Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor;
 KM Sensory transduction; Transducer; Transmembrane.
 FT TOPO_DOM 1 27
 FT TRANSMEM 28 50
 FT TOPO_DOM 51 61
 FT TRANSMEM 62 83
 FT TOPO_DOM 84 100
 FT TRANSMEM 101 121
 FT TOPO_DOM 122 140
 FT TRANSMEM 141 162
 FT TOPO_DOM 163 205
 FT TRANSMEM 206 226
 FT TOPO_DOM 227 242
 FT TRANSMEM 243 266
 FT TOPO_DOM 267 286
 FT TRANSMEM 287 306
 FT TOPO_DOM 307 349
 FT CARBOHYD 4 4
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 FT DISULFID 98 176
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 DB 1 METNFSPLNLEYEVSAGYTYTLRLPLVAVGVTVGLVGLVYVWAGPMTTYYT 60
 QY 61 TICVNLALADFSPTATLPLIVSMANGKWPFGMFLCKLIHIVVDINLFGSVLLGFIA 120

DB 61 TICVNLALADFSPTATLPLIVSMANGKWPFGMFLCKLIHIVVDINLFGSVLLGFIA 120
 QY 121 LDRICVLPVPMQONRTVSLAMKVIVGPMIALVTLFVFLPTVTIPNGDYTFNF 180
 DB 121 LDRICVLPVPMQONRTVSLAMKVIVGPMIALVTLFVFLPTVTIPNGDYTFNF 180
 QY 181 ASWGTEPERLKVATITMLTARIGIRFVIGFSLPMSIVAICYGLIAKIKKMKSRPL 240
 DB 181 PFWGDIIVVERMNVFITMAKVSILHPIIGFSIPMSIITWCYGIIVAKIKKMTKSRPL 240
 QY 241 KVTITAVASPFICWFPQVALIGTWLKMFLYGCYKTIIDIVNPTSSLAFFNSCLNPM 300
 DB 241 HITFAVASFICWFPYELTGILMAVWLBKILLNGCYKTIIVLINPTSSLAFFNSCLNPM 300
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 DB 301 LYYFVQODRERLHSLPTSLERALS--DSAPNTDANSAPPAETE 347
 RESULT 15
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 AC P21462; Q14939; Q726A4; Q86U52; Q9NS48;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE fMet-Ileu-Phe receptor (FMLP receptor) (N-formyl peptide receptor) (FPR) (N-formylpeptide chemotactant receptor).
 GN Name=PPRL;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=90267449; PubMed=2161213;
 RA Boulay F., Tardif M., Brouchon L., Vignais P.;
 RT "Synthesis and use of a novel N-formyl peptide derivative to isolate a human N-formyl peptide receptor cDNA".
 RL Biochem. Biophys. Res. Commun. 168:1103-1109(1990).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91105045; PubMed=2176894;
 RA Boulay F., Tardif M., Brouchon L., Vignais P.;
 RT "The human N-formylpeptide receptor. Characterization of two cDNA isolates and evidence for a new subfamily of G-protein-coupled receptors".
 RL Biochemistry 29:11123-11133(1990).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91286286; PubMed=1712023;
 RA Murphy P.M., McDermott D.;
 RT "Functional expression of the human formyl peptide receptor in Xenopus oocytes requires a complementary human factor".
 RL J. Biol. Chem. 266:12560-12567(1991).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=1612600;
 RA Bao L., Gerard N.P., Eddy R.L. Jr., Shows T.B., Gerard C.;
 RT "Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR), and two FMLP receptor homologue orphan receptors (FPRH1, FPRH2) to chromosome 19".
 RL Genomics 13:437-440(1992).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Perez H.D.;
 RP Submitted (MAR-1993) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=94040825; PubMed=8224916; DOI=10.1016/0378-1119(93)90653-K;
 RA Murphy P.M., Tiffany H.L., McDermott D., Ahuja S.K.;

RT "Sequence and organization of the human N-formyl peptide receptor-
 encoding gene." ;
 RL Gene 133:285-290(1993).
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANTS VAL-101; LYS-192
 AND GLU-346.
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 sequenced by the Guttrich cDNA resource center (www.cdna.org).";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP NUCLEOTIDE SEQUENCE, AND VARIANTS VAL-101 AND GLU-346.
 RA Kalnina N., Chen X., Rolfe A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J., Moreira D., Kelley T., Labber J., Lin Y.,
 RA Phelan M., Farmer A.;
 RT "Cloning of human full-length cDNAs in BD Creator(TM) system donor
 vector." ;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15057824; DOI=10.1038/nature02399;
 RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
 RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
 RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
 RA Cenepeel S., Carrano A.V., Cault C., Chan Y.M., Christensen M.,
 RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C.,
 RA Escobedo C., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,
 RA Glavina T., Gomez M., Gonzales E., Groza M., Hammond N., Hawkins T.,
 RA Hayda L., Ho I., Huang W., Izant S., Jett J., Kadner K., Kimball H.,
 RA Kobayashi S., Lartionov D., Leem S.-H., Lopez F., Lou Y., Lowry S.,
 RA Malfatti S., Martinez V., McCready P.M., Medina C., Morgan J.,
 RA Nelson K., Nolan M., Ocharenko I., Pitluck S., Pollard M.,
 RA Popkile A.P., Predki P., Qian G., Ramirez L., Rash S., Reiter J.,
 RA Rodriguez A., Rogers S., Salamon A., Salazar A., She X., Smith D.,
 RA Slezak T., Solovay V., Thayer N., Tice H., Tsal M., Uraszewski A.,
 RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
 RA Purey T.S., DeJong P., Dickson M., Gordon D., Eichler E.B.,
 RA Pennacchio L.A., Richardson P., Stubbs L., Kohner D.S., Myers R.M.,
 RA Rubin E.M., Lucas S.M.;
 RT "The DNA sequence and biology of human chromosome 19." ;
 RL Nature 428:529-535(2004).
 RN [10]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX TISSUE=Kidney; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA MEDLINE=22388257; Feingold E.A., Grouse L.H., Derge J.G.,
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tohliyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamaralle P.H.,
 RA Rickards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP NUCLEOTIDE SEQUENCE OF 1-5.
 RX PubMed=1445895;
 RA Perez H.D., Holmes R., Kelly E., McClary J., Chou Q., Andrews W.H.;
 RT "Cloning of the gene coding for a human receptor for formyl peptides.
 RT Characterization of a promoter region and evidence for polymorphic
 expression." ;

RL Biochemistry 31:11595-11599(1992).
 RN [12]
 RP PHOSPHORYLATION SITES SER-328; THR-329; THR-331; SER-332; THR-334;
 RP THR-336; SER-338 AND THR-339.
 RX MEDLINE=99445530; PubMed=10514456; DOI=10.1074/jbc.274.42.29791;
 RA Meeres D.C., Potter R.M., Prosenitz R.R.;
 RT "Differential phosphorylation paradigms dictate desensitization and
 internalization of the N-formyl peptide receptor." ;
 RL J. Biol. Chem. 274:29791-29795(1999).
 CC -1- FUNCTION: High affinity receptor for N-formyl-methionyl peptides,
 which are powerful neutrophil chemotactic factors. Binding of
 FMIP to the receptor causes activation of neutrophils. This
 response is mediated via a G-protein that activates a
 phosphatidylinositol-calcium second messenger system.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Neutrophils.
 CC -1- PTM: Phosphorylated; which is necessary for desensitization.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
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 CC EMBL: M37128; AAA36362.1; -; mRNA.
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 DR EMBL: M60627; AAA35847.1; -; mRNA.
 DR EMBL: L10820; AAA16863.1; -; Unassigned DNA.
 DR EMBL: AY301273; AAP58403.1; -; Genomic DNA.
 DR EMBL: BC007429; AAP58409.1; -; mRNA.
 DR EMBL: AC018755; AAF87842.1; -; Genomic DNA.
 DR EMBL: BC005315; AAH05315.1; -; mRNA.
 DR EMBL: S49810; AAD14906.1; -; mRNA.
 DR PIR: JC2014; A42009.
 DR Ensembl: ENSG00000171051; Homo sapiens.
 DR HGN: HGNC:3826; PPR1.
 DR H-InvDB: HIX0015389; -.
 DR MIM: 136537; -.
 DR GO: GO:0005768; Cytoplasm; TAS.
 DR GO: GO:0016021; C: integral to membrane; TAS.
 DR GO: GO:0005886; Cytoplasmic membrane; TAS.
 DR GO: GO:0004982; P: N-formyl peptide receptor activity; TAS.
 DR GO: GO:0004872; P: receptor activity; TAS.
 DR GO: GO:0000187; P: activation of MAPK; TAS.
 DR GO: GO:0006928; P: cell motility; TAS.
 DR GO: GO:0006935; P: chemotaxis; TAS.
 DR GO: GO:0007186; P: G-protein coupled receptor protein signalin...; TAS.
 DR GO: GO:0007188; P: G-protein signaling, coupled to cAMP nucle...; TAS.
 DR GO: GO:0007263; P: nitric oxide mediated signal transduction; TAS.
 DR GO: GO:0007165; P: signal transduction; TAS.
 DR InterPro: IPR000826; FcR/met receptor.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm 1; 1.
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 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G PROTEIN RECP F1_1; 1.
 DR PROSITE: PS00262; G PROTEIN RECP F1_2; 1.
 KW Chemotaxis; G-protein coupled receptor; Glycoprotein; Phosphorylation;
 KW Polymorphism; Receptor; Sensory transduction; Transducer;
 KW Transmembrane.
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 FT TOPO DOM 51 61
 FT TRANSMEM 62 83
 FT TOPO DOM 84 100
 FT TRANSMEM 101 121
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 FT TRANSMEM 141 162
 FT TOPO DOM 163 205
 FT TRANSMEM 206 226
 FT TOPO DOM 227 242
 FT TRANSMEM 243 266
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 FT 1 (Potential).
 FT Cytoplasmic (Potential).
 FT 2 (Potential).
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 FT Cytoplasmic (Potential).
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OM protein - protein search, using sw model

Run on: March 28, 2006, 13:20:18 ; Search time 62.712 Seconds
(without alignments)
462.737 Million cell updates/sec

Title: US-10-517-956-1

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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1243.5	68.4	350	1	US-07-759-568-3
5	1240.5	68.3	350	2	US-08-430-286A-8
6	1174.5	64.6	354	1	US-08-458-970A-10
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8	1117	61.5	315	4	PCT-US93-08528-34
9	626.5	34.5	135	2	US-08-513-974B-348
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15	507	27.9	350	2	US-09-826-509-467
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26	426.5	23.5	355	1	US-08-450-393A-8
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30	426.5	23.5	355	4	PCT-US95-00476-8	Sequence 8, App1
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45	419.5	23.1	352	1	US-08-076-093A-4	Sequence 4, App1

ALIGNMENTS

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; Sequence 2, Application US/09944807						
; Patent No. 6773895						
; GENERAL INFORMATION:						
; APPLICANT: Boehringer Ingelheim Pharma KG						
; TITLE OF INVENTION: Method for identifying substances which positively						
; TITLE OF INVENTION: Influence inflammatory conditions of chronic						
; FILE REFERENCE: 082.00n						
; CURRENT APPLICATION NUMBER: US/09/944,807						
; PRIOR FILING DATE: 2001-08-31						
; PRIOR APPLICATION NUMBER: UK 0021484.1						
; NUMBER OF SEQ ID NOS: 24						
; SOFTWARE: Patentin Ver. 2.1						
; SEQ ID NO 2						
; LENGTH: 351						
; TYPE: PRT						
; ORGANISM: Homo sapiens						
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Best Local Similarity 100.0%; Score 1817; DB 2; Length 351;						
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
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Db	1	METNFSPTPLNXYEVSYSASAGYTVLRILPLVVLGVTVFVLGNGLVIVWAGFRMTRTYT	60			
Qy	61	TTCTYLMALADPSFTTLPFLIVSNAMGKMPGWLCLQIHIVDINFGSVFLIGFLA	120			
Db	61	TTCTYLMALADPSFTTLPFLIVSNAMGKMPGWLCLQIHIVDINFGSVFLIGFLA	120			
Qy	121	LDRCLCVLHPVMAONRRTVSLAMKVVGPMIILVTLFVPLFLTVTIPLNGDTCTFPN	180			
Db	121	LDRCLCVLHPVMAONRRTVSLAMKVVGPMIILVTLFVPLFLTVTIPLNGDTCTFPN	180			
Qy	181	ASWGTPPEERLKVATIMLTARGIIRFVIGFSLPMSIVAICYGLIAKIKKGMKSSRPL	240			
Db	181	ASWGTPPEERLKVATIMLTARGIIRFVIGFSLPMSIVAICYGLIAKIKKGMKSSRPL	240			
Qy	241	RVTAVVASPFICWPFQVALIGTWLKKMLFYGKTKIIDILVNPTSSLAFFNSCLANP	300			
Db	241	RVTAVVASPFICWPFQVALIGTWLKKMLFYGKTKIIDILVNPTSSLAFFNSCLANP	300			
Qy	301	LVYFVQDPRERIRHSLPTSLERALSDESAPTNDTANASAPPAETELQAM	351			
Db	301	LVYFVQDPRERIRHSLPTSLERALSDESAPTNDTANASAPPAETELQAM	351			

```
RESULT 2
US-09-826-509-501
; Sequence 501, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Brulnema, Karin
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patentin Version 2.1
; SEQ ID NO 501
; LENGTH: 351
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-826-509-501

Query Match          99.7%; Score 1811; DB 2; Length 351;
Best Local Similarity 99.7%; Pred. No. 2.6e-126;
Matches 350; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 METNFSPLNEXBEVSYESAGYVLRILPLVLTGTFVGLGNGLYVWAGFRMTRTYT 60
DB 1 METNFSPLNEXBEVSYESAGYVLRILPLVLTGTFVGLGNGLYVWAGFRMTRTYT 60
QY 61 TICYLNLALADSFATLPFLIVSMAMGKMPFGFLCKLIHIVDINLFGSVFLIGFTA 120
DB 61 TICYLNLALADSFATLPFLIVSMAMGKMPFGFLCKLIHIVDINLFGSVFLIGFTA 120
QY 121 LDRICVILHPVMAQNHRVTSIAKVIIGVPIIALVLTLPVFLPLTTVTIPNGDYCTENF 180
DB 121 LDRICVILHPVMAQNHRVTSIAKVIIGVPIIALVLTLPVFLPLTTVTIPNGDYCTENF 180
QY 121 LDRICVILHPVMAQNHRVTSIAKVIIGVPIIALVLTLPVFLPLTTVTIPNGDYCTENF 180
DB 121 LDRICVILHPVMAQNHRVTSIAKVIIGVPIIALVLTLPVFLPLTTVTIPNGDYCTENF 180
QY 181 ASWGGTPEERLKVATIMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
DB 181 ASWGGTPEERLKVATIMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
QY 181 ASWGGTPEERLKVATIMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
DB 181 ASWGGTPEERLKVATIMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
QY 241 RVLTAIVASFFICWPPQVALIGTWMLKEMLFYKXKIIDIIVNPTSSIAFPNSCLNPM 300
DB 241 RVLTAIVASFFICWPPQVALIGTWMLKEMLFYKXKIIDIIVNPTSSIAFPNSCLNPM 300
QY 241 RVLTAIVASFFICWPPQVALIGTWMLKEMLFYKXKIIDIIVNPTSSIAFPNSCLNPM 300
DB 241 RVLTAIVASFFICWPPQVALIGTWMLKEMLFYKXKIIDIIVNPTSSIAFPNSCLNPM 300
QY 301 LVYFVGODFRERLIHSLPTSLERALSSEDSAPTNDTANASAPPAETELQAM 351
DB 301 LVYFVGODFRERLIHSLPTSLERALSSEDSAPTNDTANASAPPAETELQAM 351

RESULT 3
US-09-826-509-499
; Sequence 499, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Brulnema, Karin
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
```

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; SOFTWARE: Patentin Version 2.1
; SEQ ID NO 499
; LENGTH: 350
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-826-509-499

Query Match          68.6%; Score 1244.5; DB 2; Length 350;
Best Local Similarity 68.6%; Pred. No. 1.7e-84;
Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps 1;

QY 1 METNFSPLNEXBEVSYESAGYVLRILPLVLTGTFVGLGNGLYVWAGFRMTRTYT 60
DB 1 METNFSPLNEXBEVSYESAGYVLRILPLVLTGTFVGLGNGLYVWAGFRMTRTYT 60
QY 61 TICYLNLALADSFATLPFLIVSMAMGKMPFGFLCKLIHIVDINLFGSVFLIGFTA 120
DB 61 TICYLNLALADSFATLPFLIVSMAMGKMPFGFLCKLIHIVDINLFGSVFLIGFTA 120
QY 61 TICYLNLALADSFATLPFLIVSMAMGKMPFGFLCKLIHIVDINLFGSVFLIGFTA 120
DB 61 TICYLNLALADSFATLPFLIVSMAMGKMPFGFLCKLIHIVDINLFGSVFLIGFTA 120
QY 121 LDRICVILHPVMAQNHRVTSIAKVIIGVPIIALVLTLPVFLPLTTVTIPNGDYCTENF 180
DB 121 LDRICVILHPVMAQNHRVTSIAKVIIGVPIIALVLTLPVFLPLTTVTIPNGDYCTENF 180
QY 121 LDRICVILHPVMAQNHRVTSIAKVIIGVPIIALVLTLPVFLPLTTVTIPNGDYCTENF 180
DB 121 LDRICVILHPVMAQNHRVTSIAKVIIGVPIIALVLTLPVFLPLTTVTIPNGDYCTENF 180
QY 181 ASWGGTPEERLKVATIMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
DB 181 ASWGGTPEERLKVATIMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
QY 181 ASWGGTPEERLKVATIMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
DB 181 ASWGGTPEERLKVATIMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKGMKSSRPL 240
QY 241 RVLTAIVASFFICWPPQVALIGTWMLKEMLFYKXKIIDIIVNPTSSIAFPNSCLNPM 300
DB 241 RVLTAIVASFFICWPPQVALIGTWMLKEMLFYKXKIIDIIVNPTSSIAFPNSCLNPM 300
QY 241 RVLTAIVASFFICWPPQVALIGTWMLKEMLFYKXKIIDIIVNPTSSIAFPNSCLNPM 300
DB 241 RVLTAIVASFFICWPPQVALIGTWMLKEMLFYKXKIIDIIVNPTSSIAFPNSCLNPM 300
QY 301 LVYFVGODFRERLIHSLPTSLERALSSEDSAPTNDTANASAPPAETELQAM 350
DB 301 LVYFVGODFRERLIHSLPTSLERALSSEDSAPTNDTANASAPPAETELQAM 349
```

```
RESULT 4
US-07-759-568-3
; Sequence 3, Application US/07759568
; Patent No. 5374506
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
; TITLE OF INVENTION: Human Interleukin-8 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,568
; FILING DATE: 19910913
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 cush
; INFORMATION FOR SEQ ID NO. 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: AMINO ACID
```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-759-568-3

Query Match 68.4%; Score 1243.5; DB 1; Length 350;
Best Local Similarity 68.6%; Pred. No. 2.1e-84;
Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps 1;

QY 1 METNFTPLNEBESVESAGYTVLRILPLVVLGTVFLGNGLVIVVAGFRMTT 60
DB 1 METNFTPLNEBESVESAGYTVLRILPLVVLGTVFLGNGLVIVVAGFRMTT 60
QY 61 TICLYNLALADSFATLPLPLIVSMANGKMPGKFLCLIHIVDINLFGSVFLIGFLA 120
DB 61 TICLYNLALADSFATLPLPLIVSMANGKMPGKFLCLIHIVDINLFGSVFLIGFLA 120
QY 121 LDRICVLHPVWAQNHRVSLAMKVIIGPWWIALVLTLPVFLPTVTIENGDTCTFNF 180
DB 121 LDRICVLHPVWAQNHRVSLAMKVIIGPWWIALVLTLPVFLPTVTIENGDTCTFNF 180
QY 181 ASWGTPEERLKYAITMLTARGIIRFVIGSLPMSIYVAICGLIAKIHKKMIKSRPL 240
DB 181 ASWGTPEERLKYAITMLTARGIIRFVIGSLPMSIYVAICGLIAKIHKKMIKSRPL 240
QY 241 RVLTAVASFPICMPFQVALGTVLWKEMLFYGYKIIDILVNPTSSLAFNSCLNPM 300
DB 241 RVLTAVASFPICMPFQVALGTVLWKEMLFYGYKIIDILVNPTSSLAFNSCLNPM 300
QY 301 LVYFVGQDFRERLIHSLPFLERALSDESAPTNDTANASAPPAETELQA 350
DB 301 LVYFVGQDFRERLIHSLPFLERALSDESAPTNDTANASAPPAETELQA 350

RESULT 5
US-08-430-286A-8
Sequence 8, Application US/08430286A

GENERAL INFORMATION:
PATENT No. 6225080
APPLICANT: Unl, George R.
APPLICANT: Eppier, C. Mark
APPLICANT: Wang, Jai-Bel
TITLE OF INVENTION: Mu-Subtype Opioid Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,286A
FILING DATE: 28-APR-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Roblinson, Joseph R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1A843-US5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: P-REP
US-08-430-286A-8

Query Match 68.3%; Score 1240.5; DB 2; Length 350;
Best Local Similarity 68.6%; Pred. No. 3.4e-84;
Matches 240; Conservative 37; Mismatches 72; Indels 1; Gaps 1;

QY 1 METNFTPLNEBESVESAGYTVLRILPLVVLGTVFLGNGLVIVVAGFRMTT 60
DB 1 METNFTPLNEBESVESAGYTVLRILPLVVLGTVFLGNGLVIVVAGFRMTT 60
QY 61 TICLYNLALADSFATLPLPLIVSMANGKMPGKFLCLIHIVDINLFGSVFLIGFLA 120
DB 61 TICLYNLALADSFATLPLPLIVSMANGKMPGKFLCLIHIVDINLFGSVFLIGFLA 120
QY 121 LDRICVLHPVWAQNHRVSLAMKVIIGPWWIALVLTLPVFLPTVTIENGDTCTFNF 180
DB 121 LDRICVLHPVWAQNHRVSLAMKVIIGPWWIALVLTLPVFLPTVTIENGDTCTFNF 180
QY 181 ASWGTPEERLKYAITMLTARGIIRFVIGSLPMSIYVAICGLIAKIHKKMIKSRPL 240
DB 181 ASWGTPEERLKYAITMLTARGIIRFVIGSLPMSIYVAICGLIAKIHKKMIKSRPL 240
QY 241 RVLTAVASFPICMPFQVALGTVLWKEMLFYGYKIIDILVNPTSSLAFNSCLNPM 300
DB 241 RVLTAVASFPICMPFQVALGTVLWKEMLFYGYKIIDILVNPTSSLAFNSCLNPM 300
QY 301 LVYFVGQDFRERLIHSLPFLERALSDESAPTNDTANASAPPAETELQA 350
DB 301 LVYFVGQDFRERLIHSLPFLERALSDESAPTNDTANASAPPAETELQA 350

RESULT 6
US-08-458-970A-10
Sequence 10, Application US/08458970A

GENERAL INFORMATION:
PATENT No. 5861272
APPLICANT: LI, ET AL.
TITLE OF INVENTION: C5a Receptor
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARBELL, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,970A
FILING DATE: June 2, 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 10:


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QY 114 FLIGIALDRICVLAHPVAOKHRTSLAMKVIYGVPMIALVLTLPVPLFTVTIPNG 173
Db 125 LLMATISDRFLVAVKPIICQNPFRAGLAMIACVAMGALALLTISFLYRV-----RE 179
-QY 174 TY-----CTENFASMGGTPEERLKAVALTMTARGLIRFVIGSPLSMSTVAICYGLIAAK 227
Db 180 EYFPKVLGVDYSH-----DKRRERAV-----AIVRLVLGFLWELTLTYCTFLIR 228
QY 228 IHKKGMIKSRRLRYLTVAASFICMPPEOLVALLGTWLBKMLPYGKKIIDILVNP 287
Db 229 TWSRATSTKTLKVVAVVASFILFMLPYQTGIN-----MSTLEBSSPFLILANTL 281
QY 288 SSL-----AFNSCLNPMULVFPVGDPRERLISLPTSLERALSDESA-----PTND 334
Db 282 DSLGVSFAYINCCINPIIYVAVGQGFQGLRSLSLRNVLNVLTEESVRESKSFTRSTVD 341
QY 335 TAA 337
Db 342 TMA 344

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RESULT 13
US-09-117-440-2
; Sequence 2, Application US/09117440
; Patent No. 6521418
; GENERAL INFORMATION:
; APPLICANT: Ye, Richard D
; TITLE OF INVENTION: A G PROTEIN-COUPLED RECEPTOR WITH AN ENLARGED
; TITLE OF INVENTION: EXTRACELLULAR DOMAIN
; FILE REFERENCE: SCR20415
; CURRENT APPLICATION NUMBER: US/09/117,440
; CURRENT FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: PCT/US97/01736
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: 60/010,808
; EARLIER FILING DATE: 1996-01-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Human
; US-09-117-440-2

```

Query Match	28.0%	Score 509.5	DB 2	Length 482
Best Local Similarity	26.6%	Pred. No. 4.4e-30		
Matches 134	Conservative 59	Mismatches 117	Indels 193	Gaps 11
QY	2	ETN-----FSTPLNEXEVSYSAGYTVARILPLVVLGYTVGLVGNGLVIVWVAGFMRTR	57	
Db	7	ETNSTDLLSQWNEPVPV-----ILSMVLISLTPLGLGNGGLVWVAGLKNQR	54	
QY	58	TVTITTCYINLMLADPSFTATPLPLIVSNMAGKEKPFQFLCKLHIYVDINLFGSVELIG	117	
Db	55	TVNTIWFHLTLADLLCCLSLPFSLHMLADLGOMWYGRFLCKLPSIIVLNMFAVSFILLT	114	
QY	118	FIATDRICVLAHPWAONHRTVYSLAMKVIYGVFWLALVLTLPVPLFTVTIVIPNDYCT	177	
Db	115	AIISDRCLVYKFPILWQONHRVNGACISIGCCIWVAFWMCIFVFEYREIPTTDNHR-CG	173	
QY	178	FNFA-----SW-----	183	
Db	174	YKFGILSSLDYDPFYGDPLENRSLENIVQRPGENMDRLDPSFQTNHHPVTVTFQRPQT	233	
QY	184	-----CGTBE-----R	190	
Db	234	FORESADSLPRGSARLTSQNLVSNVFEADYVSPKIPSGFPIEDHETSPLDNSDAFLSTH	293	
QY	191	LKV-----AITMLTARGLIRRVIGSGPMSIVIA	218	
Db	294	LKLPSPSASNSFYSESLPEQGFODIYVNLGQFTDDDDVPPPLVAITITRLVAVGFLPSVIMT	353	

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Oy      219  ICGGLAAIIHKKKIMK-SRPLRLTVAASFFICMPFQVALLGVMLEKMLFYGY 277
      219  ::::: ||| ||| :::::
Db      354  ACTSFIVFMQGRFPAKSQKTFRAVVVVAFLVCTPYII-----F 356
      354  ::::: ||| ||| :::::
Oy      278  KIIDLVNPTS-----SLAFNSCLNPMLYEVGODPFRRLIHSPTSLE 323
      278  ::::: ||| ||| :::::
Db      397  GVLSLTIDETPLGKTIISMDBVCIALLAANSNCRPFYALLGKDFKKARQSIQIILE 456
      397  ::::: ||| ||| :::::
Oy      324  ALSED-----SAPTNDTAAANSAS 341
      324  ||::: ||::: ||:::
Db      457  AFSEELTRTHCPSSNNVVISERN 479

```

RESULT 14
US-08-876-874-2
Sequence 2, Application US/08876874
Patent No. 5943405
GENERAL INFORMATION:
APPLICANT: Ames, Robert
APPLICANT: Bergsma, Derk
APPLICANT: Foley, James
APPLICANT: Kumar, Chandrika
APPLICANT: Saracu, Henry
TITLE OF INVENTION: THERAPEUTIC AND SCREENING
TITLE OF INVENTION: METHODS USING C3A RECEPTOR AND C3A
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: 5

```

1 STREET: P.O. BOX 980
2 CITY: VALLEY FORGE
3 STATE: PA
4 COUNTRY: USA
5 ZIP: 19482
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Diskette
8 COMPUTER: IBM Compatible
9 OPERATING SYSTEM: DOS
10 SOFTWARE: FastSEO for Windows Version 2.0
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: US/08/876,874
13 FILING DATE:
14 CLASSIFICATION: 536
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: 60/019,627
17 FILING DATE: 16-JUN-1997
18 ATTORNEY/AGENT INFORMATION:
19 NAME: PRESTIA, PAUL F
20 REGISTRATION NUMBER: 23,031
21 REFERENCE/DOCKET NUMBER: P50501
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: 610-407-0700
24 TELEFAX: 610-407-0701
25 TELEX: 846169
26 INFORMATION FOR SEQ ID NO: 2:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 482 amino acids
29 TYPE: amino acid
30 STRANDEDNESS: single
31 TOPOLOGY: linear
32 MOLECULE TYPE: protein
33 JS-08-876-874-2

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[illegible]

QY 118 FIALDRICICVLHPVMAQNHRTVSLAMKVIQVPMIALVLTLPVFLFTVTITINGDTYCT 177
 Db 115 AILSDRCLVFKPIWQNHRTVSGACISICGCIWVAVCMCIPIVAVREIPTDNHR-CG 173
 QY 178 FNA-----SN----- 183
 Db 174 YKGLASSLDDPDYGDPLENRSLENIWOPGEMNDRLDSSFOQNDHPMTVPTVPOPT 233
 QY 184 -----GTPRE-----R 190
 Db 234 FQRPASDLSLRGSAKLTSQNLVSNVFKPADVSPKIPSGPIIDHESPLDNDALFSTH 293
 QY 191 LKV-----ALMTLARGIIRFYIGFSLPMSTVA 218
 Db 294 LKLPFASNSPYESELPGQFQDYNNLQFTDDQVPTPLVALITRILVVGFLPSVIMI 353
 QY 219 ICGGLAAKIKHKGMKIS-SRPLRVLTAVVASFFICFPQVALLGTWLEKMLFYGKT 277
 Db 354 ACSFVIFRQGRFPAKSQSKTRFVAVVAVFLVCMTPYHI-----F 396
 QY 278 KIIDIIVNPTS-----SLAFNSCLNPMLYVVGODFRERLHSLPTSLER 323
 Db 397 GVLSLTIDPETPKGKILMSWDHVCIALASNSCFNPFLVALKGRKAKROSIGILEA 456
 QY 324 ALSED-----SAPTNDTAANSAS 341
 Db 457 AFSEELTRSTHCPSSNNVISERNIS 479

RESULT 15
 US-09-826-509-467
 ; Sequence 467, Application US/09826509
 ; Patent No. 6806054
 ; GENERAL INFORMATION:
 ; APPLICANT: Lehmann-Brulnema, Karin
 ; APPLICANT: Liaw, Chen W.
 ; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
 ; TITLE OF INVENTION: Protein-Coupled Receptors
 ; FILE REFERENCE: AREN-207
 ; CURRENT APPLICATION NUMBER: US/09/826,509
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/195,747
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: 09/170,496
 ; PRIOR FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 589
 ; SOFTWARE: Patent Version 2.1
 ; SEQ ID NO 467
 ; LENGTH: 350
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-826-509-467

Query Match 27.9%; Score 507; DB 2; Length 350;

Best Local Similarity 33.3%; Pred. No. 4.9e-30;

Matches 121; Conservative 60; Mismatches 130; Indels 52; Gaps 9;

QY 4 NSTP-LNVEE-----VYESAGTVVLRILPLVVLGTVFVLGNGLVTVVAGF 53
 Db 5 NYTPDYGYDDDTLDLNTPTVDKTSNTLRVPDILALVFAVFLVGLGNALVWVWTA 64
 QY 54 RMTRTVTTCYLNALADPSFTATLPFLVSMAMEKMPGWFGLCKLIHVVDINFGSV 113
 Db 65 EAKRTINAWFLNALAVADPLSCIALPILTSIVQHHMPGAGACSLPSLIILNNYASI 124
 QY 114 FLIGFIALDRICICVLHPVMAQNHRTVSLAMKVIQVPMIALVLTLPVFLFTVTIPNGD 173
 Db 125 LILATISADRPILVFKPIWQNHRTVSGACISICGCIWVAVCMCIPIVAVREIPTDNHR-CG 173
 QY 174 TY-----CTNFASWGGTPEERLKAITMLTARGIIRFYIGFSLPMSTVAICYGLIAAK 227

Db 180 EYFPKVLGVDYSH-----DKRRERAV-----ALVRLVGLFWPLTLTITCTPIILR 228
 QY 228 IHKGMKISSRPLRVLTAVVASFFICFPQVALLGTWLEKMLFYGKYKIDILVNPT 287
 Db 229 TWSRATRSTKTKKVAVVASFFIFMLPYQTGIN-----MSFLBESSPTPLINKL 281
 QY 288 SSL-----AFNSCLNPMLYVVGODFRERLHSLPTSLERALSOSA-----PTWD 334
 Db 282 DSLCVSFAYINCINPIIYVAGOGFQGRLRKSLPSLLENVLTESSVRESKSPTRSTVD 341
 QY 335 TAA 337
 Db 342 TMA 344

Search completed: March 28, 2006, 13:22:08
 Job time : 63.712 secs